Myers
09/673645

FILE 'REGISTRY' ENTERED AT 12:30:46 ON 09 SEP 2002
L1 2 S CGGGGTCTTCCCGTCTT/SQSN

L1 ANSWER 1 OF 2 REGISTRY COPYRIGHT 2002 ACS
RN 288698-77-1 REGISTRY
CN GenBank AX009453 (9CI) (CA INDEX NAME)
CI MAN
SQL 17

SEQ 1 cggggtcttc ccgtctt
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HITS AT: 1-17

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L1 ANSWER 2 OF 2 REGISTRY COPYRIGHT 2002 ACS
RN 251931-90-5 REGISTRY
CN DNA, d(C-G-G-G-G-T-C-T-T-C-C-C-G-T-C-T-T) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 11: PN: WO9961660 SEQID: 1 claimed sequence
CI MAN
SQL 17

SEQ 1 cggggtcttc ccgtctt
========== =======
HITS AT: 1-17

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 132:20800

FILE 'HCAPLUS' ENTERED AT 12:31:52 ON 09 SEP 2002
L2 1 S L1

L2 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:764237 HCAPLUS
DOCUMENT NUMBER: 132:20800
TITLE: Determination of antibiotic resistance of microorganisms by in situ hybridization using mutation-specific 23S rRNA-targetted oligonucleotide probes
INVENTOR(S): Haas, Rainer; Trebesius, Karlheinz; Apfel, Heiko
PATENT ASSIGNEE(S): Creatogen Biosciences G.m.b.H., Germany
SOURCE: PCT Int. Appl., 84 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9961660	A1	19991202	WO 1999-EP3527	19990521

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG,

SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW,
AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE,
DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ,
CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

DE 19916610	A1	19991125	DE 1999-19916610	19990413
CA 2329057	AA	19991202	CA 1999-2329057	19990521
AU 9942658	A1	19991213	AU 1999-42658	19990521
BR 9910646	A	20010130	BR 1999-10646	19990521
EP 1078104	A1	20010228	EP 1999-938039	19990521
R: AT, BE, CH, DE, DK, ES, FR, GB, IT, LI, NL, SE, IE				
JP 2002516665	T2	20020611	JP 2000-551040	19990521

PRIORITY APPLN. INFO.: DE 1998-19823098 A 19980522
DE 1999-19916610 A 19990413
WO 1999-EP3527 W 19990521

AB The invention concerns the detn. of bacterial antibiotic resistance by in situ hybridization using a combination of at least two mutation-specific 23S rRNA-targetted oligonucleotide probes, along with probes that are targetted to E.coli homologous regions of Heliobacter pylori 16S rRNA. Probes are fluorescent or enzyme labeled; samples are tissues or body fluids; microorganisms are isolated; detected without culturing or cultured; cell walls are made permeable; and nucleic acids are isolated for in situ hybridization. Fluorescence microscopy is used for detection. Helicobacter species, Mycobacteria, Chlamydia, etc. can be identified and the antibiotic resistance detd. by the method. Resistance to macrolides, lincosamide, aminoglycosides, aminocyclitol, tetracycline and chloramphenicol can be detected. The invention also concerns a test kit contg. the necessary reagents and probes.

IT **251931-90-5**
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(hybridization probe ClaR1 for H.pylori A2058G ClaR, 23S 2051-2067 region-specific; detn. of antibiotic resistance of microorganisms by in situ hybridization using mutation-specific 23S rRNA-targetted oligonucleotide probes)

REFERENCE COUNT: 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

(FILE 'MEDLINE' ENTERED AT 12:32:49 ON 09 SEP 2002)

L3 1224 SEA FILE=MEDLINE ABB=ON PLU=ON "RNA, RIBOSOMAL, 23S"/CT
L4 454 SEA FILE=MEDLINE ABB=ON PLU=ON HELICOBACTER/CT
L5 3 SEA FILE=MEDLINE ABB=ON PLU=ON L3 AND L4

-Key terms

L5 ANSWER 1 OF 3 MEDLINE
AN 2002296754 MEDLINE
TI Captive rhesus monkeys (Macaca mulatta) are commonly infected with Helicobacter cinaedi.
AU Fernandez Kathy R; Hansen Lori M; Vandamme Peter; Beaman Blaine L; Solnick Jay V
SO JOURNAL OF CLINICAL MICROBIOLOGY, (2002 Jun) 40 (6) 1908-12. Journal code: 7505564. ISSN: 0095-1137.
AB Helicobacter cinaedi may cause proctocolitis or bacteremia in homosexual men infected with human immunodeficiency virus or

occasionally in other immunocompromised hosts. There are scattered reports of H. cinaedi isolated from a variety of animal hosts, but to date only hamsters have been found to be a common natural reservoir. Microaerophillic cultures of feces from 5 of 16 asymptomatic rhesus monkeys (Macaca mulatta) (31%) were positive for a curved gram-negative rod. A polyphasic taxonomic approach was used to identify the organism as H. cinaedi. These results show that H. cinaedi frequently colonizes asymptomatic captive rhesus monkeys, which may serve as another potential reservoir for human infection.

L5 ANSWER 2 OF 3 MEDLINE
AN 1999228908 MEDLINE
TI Evaluation of a molecular identification scheme based on 23S rRNA gene polymorphisms for differentiating canine and feline gastric Helicobacter spp.
AU Jalava K; Hielm S; Hirvi U; Hanninen M L
SO LETTERS IN APPLIED MICROBIOLOGY, (1999 Apr) 28 (4) 269-74.
Journal code: 8510094. ISSN: 0266-8254.
AB A scheme for the rapid identification of Helicobacter spp. using restriction fragment length polymorphism digestion profiles of PCR amplified 23S rRNA genes is described. The efficacy of this scheme for speciation of the closely related gastric species H. felis, H. bizzozeronii and H. salomonis was evaluated. It was difficult to distinguish between some RFLP profiles obtained and often, more than one profile was seen with each species examined. Some evidence was found that the 23S rRNA gene copies of these species may not be identical. Moreover, the identification scheme was ineffective in discriminating these species from each other, although they could be differentiated, as a group, from other Helicobacter spp. The results indicate that this scheme should be carefully evaluated with a number of isolates if it is to be applied to additional, highly related Helicobacter spp.

L5 ANSWER 3 OF 3 MEDLINE
AN 97409959 MEDLINE
TI Sequence similarities between large subunit ribosomal RNA gene intervening sequences from different Helicobacter species.
AU Hurtado A; Clewley J P; Linton D; Owen R J; Stanley J
SO GENE, (1997 Jul 18) 194 (1) 69-75.
Journal code: 7706761. ISSN: 0378-1119.
AB When the 23S rRNA genes from several Helicobacter species were amplified by PCR and compared with similar amplicons derived from H. pylori, they were seen to be enlarged in size. Sequencing of these enlarged genes from H. mustelae, H. canis (two strains) and H. muridarum identified insertions of novel sequence (intervening sequences, IVSs) sized between 93 and 377 bp located at nt 545, in place of an 8-nt sequence in the conventionally sized H. pylori gene. These IVSs were not present elsewhere in the genome. All strains with such IVSs lacked intact 23S rRNA which was replaced by two fragment whose sizes were consistent with cleavage at either side of the particular IVS. The predicted secondary structures of the four IVSs were characterised by base pairing at the 5' and 3' ends to form a stem. The four IVSs exhibited significant sequence inter-relationships. Further relationships were also observed between them and similar elements in both small and large subunit rRNA genes of other Helicobacter and Campylobacter species. Alignment of each IVS with the other such elements identified blocks of related sequence consistent with insertion/deletion events,

indicating possible evolutionary relationships.

FILE 'HOME' ENTERED AT 12:33:48 ON 09 SEP 2002

Searcher : Shears 308-4994

Myers
09/673645

09sep02 11:08:43 User219783 Session D1867.2

SYSTEM:OS - DIALOG OneSearch
File 440:Current Contents Search(R) 1990-2002/Sep 09
(c) 2002 Inst for Sci Info
File 34:SciSearch(R) Cited Ref Sci 1990-2002/Sep W2
(c) 2002 Inst for Sci Info
*File 34: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.
File 5:Biosis Previews(R) 1969-2002/Sep W1
(c) 2002 BIOSIS
*File 5: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.
File 155:MEDLINE(R) 1966-2002/Sep W1
*File 155: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.
File 73:EMBASE 1974-2002/Aug W4
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*File 73: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.
File 399:CA SEARCH(R) 1967-2002/UD=13710
(c) 2002 American Chemical Society
*File 399: Use is subject to the terms of your user/customer agreement. Alert feature enhanced for multiple files, etc. See HELP ALERT.
File 144:Pascal 1973-2002/Sep W2
(c) 2002 INIST/CNRS
File 76:Life Sciences Collection 1982-2002/Aug
(c) 2002 Cambridge Sci Abs
File 348:EUROPEAN PATENTS 1978-2002/Sep W01
(c) 2002 European Patent Office
File 162:CAB HEALTH 1983-2002/Jul
(c) 2002 CAB INTERNATIONAL
*File 162: Truncating CC codes is recommended for full retrieval. See Help News162 for details.
File 50:CAB Abstracts 1972-2002/Aug
(c) 2002 CAB International
*File 50: Truncating CC codes is recommended for full retrieval. See Help News50 for details.
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File 94:JICST-EPlus 1985-2002/Jul W2
(c)2002 Japan Science and Tech Corp(JST)
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File 98:General Sci Abs/Full-Text 1984-2002/Jul
(c) 2002 The HW Wilson Co.
File 156:ToxFile 1965-2002/Sep W1
(c) format only 2002 The Dialog Corporation
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*File 351: Alerts can now have images sent via all delivery methods.
See HELP ALERT and HELP PRINT for more info.
  File  16:Gale Group PROMT(R)  1990-2002/Sep 09
        (c) 2002 The Gale Group
*File  16: Alert feature enhanced for multiple files, duplicate
removal, customized scheduling. See HELP ALERT.
  File 172:EMBASE Alert  2002/Sep W1
        (c) 2002 Elsevier Science B.V.
  File 229:Drug Info. Fulltext  2002
        (c) 2002 Ameri.Soc.of Health-Systems Pharm.
  File 357:Derwent Biotech Res.  1982-2002/June W1
        (c) 2002 Thomson Derwent & ISI
*File 357: File enhancements now online. See HELP NEWS 357.
Alert feature enhanced for multiple files, etc. See HELP ALERT.
  File 370:Science  1996-1999/Jul W3
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  File 444:New England Journal of Med.  1985-2002/Sep W2
        (c) 2002 Mass. Med. Soc.
  File  10:AGRICOLA  70-2002/Aug
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  File  65:Inside Conferences  1993-2002/Sep W2
        (c) 2002 BLDSC all rts. reserv.
  File 129:PHIND(Archival)  1980-2002/Sep W1
        (c) 2002 PJB Publications, Ltd.
  File 174:Pharm-line(R)  1978-2002/Sep W1
        (c) CROWN COPYRIGHT 2002
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There is no data missing.
  File 266:FEDRIP  2002/Jul
       Comp & dist by NTIS, Intl Copyright All Rights Res
  File 315:ChemEng & Biotec Abs  1970-2002/Jul
        (c) 2002 DECHEMA
  File 358:Current BioTech Abs  1983-2001/Oct
        (c) 2001 DECHEMA
*File 358: Updates delayed. Please see HELP NEWS 358 for details.
  File 442:AMA  Journals  1982-2002/Aug B1
        (c)2002 Amer Med Assn -FARS/DARS apply
  File 484:Periodical Abs Plustext  1986-2002/Sep W1
        (c) 2002 ProQuest
*File 484: SELECT IMAGE AVAILABILITY FOR PROQUEST FILES
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      Set  Items  Description
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-key terms

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Set     Items   Description
S10     14587   (23S OR 23(W)S)(5N)(RRNA OR (RIBOSOM? OR R)(W)(RNA OR RIBO-
             NUCLEIC OR RIBO(W)NUCLEIC))
S11       766   S10 AND (HELICOBACTER? OR PYLORI)
S12       627   S11 AND (MUTAT? OR MUTAGEN? OR MUTANT? ? OR POLYMORPH? OR -
             POLY(W)(MORPHIC? OR MORPHISM? ?))
S13       278   S12 AND ANTIBIOT?(5N)RESIST?
S14       177   S13 AND (DETECT? OR DETERM? OR DET?? OR SCREEN?)
S15        62   RD (unique items)
>>>No matching display code(s) found in file(s): 65, 129, 229, 453

 15/3,AB/1     (Item 1 from file: 440)
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DIALOG(R)File 440:Current Contents Search(R)

14417512 Document Delivery Available: 000177188300014 References: 21
TITLE: Antibiotic susceptibility of *Helicobacter"** *pylori"** in Germany: stable primary resistance from 1995 to 2000
AUTHOR(S): Wolle K; Leodolter A; Malfertheiner P; Konig W (REPRINT)
AUTHOR(S) E-MAIL: wolfgang.koenig@medizin.unimagdeburg.de
CORPORATE SOURCE: Otto Von Guericke Univ, Inst Med Microbiol, /Magdeburg//Germany/ (REPRINT); Otto Von Guericke Univ, Inst Med Microbiol, /Magdeburg//Germany/; Otto Von Guericke Univ, Dept Gastroenterol Hepatol & Infect Dis, /Magdeburg//Germany/
PUBLICATION TYPE: JOURNAL
PUBLICATION: JOURNAL OF MEDICAL MICROBIOLOGY, 2002, V51, N8 (AUG), P705-709
GENUINE ARTICLE#: 579QA
PUBLISHER: LIPPINCOTT WILLIAMS & WILKINS, 530 WALNUT ST, PHILADELPHIA, PA 19106-3621 USA
ISSN: 0022-2615
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: The issue of *antibiotic"** *resistance"** in *Helicobacter"** *pylori"** is of particular concern and has become an important factor leading to eradication failure. This paper reports the prevalence of primary resistance to clarithromycin, amoxicillin, metronidazole and tetracycline among H. *pylori"** isolates in the north-eastern part of Germany. A total of 1644 clinical H. *pylori"** isolates was investigated over a period of 6 years from 1995 to 2000. The MICs were *determined"** by the Etest. The overall rate of primary resistance was 26.2% for metronidazole and 2.2% for clarithromycin. No significant changes in the resistance rates during the period of investigation were observed. No isolate was resistant to amoxicillin or tetracycline. PCR-RFLP analysis for the *detection"** of point *mutations"** associated with clarithromycin resistance was performed with 36 H. *pylori"** isolates. The A --> G transition *mutation"** at position 2143 was *detected"** in 19 H. *pylori"** isolates (52.8%), whereas the *mutation"** at position 2142 was found in 13 isolates (36.1%).

15/3,AB/2 (Item 2 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

13993344 Document Delivery Available: 000175662800066 References: 27
TITLE: *Helicobacter"** *pylori"** primary resistance to metronidazole and clarithromycin in Brazil
AUTHOR(S): Magalhaes PP; Queiroz DMD (REPRINT); Barbosa DVC; Rocha GA; Mendes EN; Santos A; Correa PRV; Rocha AMC; Teixeira LM; de Oliveira CA
AUTHOR(S) E-MAIL: dqueiroz@medicina.ufmg.br
CORPORATE SOURCE: UFMG, Lab Bacteriol, Av Alfredo Balena 190 Sala 4026/BR-30130100 Belo Horizonte/MG/Brazil/ (REPRINT); UFMG, Lab Bacteriol, /BR-30130100 Belo Horizonte/MG/Brazil/; Univ Itauna, Fac Fisioterapia, /Itauna/MG/Brazil/; Univ Fed Rio de Janeiro, Inst Microbiol, /Rio De Janeiro//Brazil/
PUBLICATION TYPE: JOURNAL
PUBLICATION: ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, 2002, V46, N6 (JUN), P 2021-2023
GENUINE ARTICLE#: 553EM
PUBLISHER: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904

USA
ISSN: 0066-4804
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: *Helicobacter"** *pylori"** resistance to metronidazole was *detected"** in 107 (52.97%) of 202 strains. Twenty (9.85%) strains, IS of them harboring 23S ribosomal DNA *mutations"**, were resistant to clarithromycin. Metronidazole resistance was associated with female gender. Resistance to metronidazole and resistance to clarithromycin were associated. Increasing clarithromycin resistance rates were observed over time.

15/3,AB/3 (Item 3 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

13565517 Document Delivery Available: 000174277400005 References: 26
TITLE: Acquisition of secondary resistance after a first course failure of treatment of *Helicobacter"** *pylori"** infection in children
AUTHOR(S): Kalach N; Benhamou PH; Bergeret M; Gottrand F; Husson MO; Barbier C; Dupont C; Raymond J (REPRINT)
AUTHOR(S) E-MAIL: j.raymond@svp.ap-hop-paris.fr
CORPORATE SOURCE: Hop St Vincent de Paul, Serv Pediat, 82 Ave Denfert Rochereau/F-75674 Paris 14//France/ (REPRINT); Hop St Vincent de Paul, Serv Pediat, /F-75674 Paris 14//France/; Hop St Vincent de Paul, Serv Bacteriol, /F-75674 Paris//France/; Univ Catholique Lille, Serv Pediat, /F-59000 Lille//France/; CHRU Lille, Serv Pediat, /F-59000 Lille//France/
PUBLICATION TYPE: JOURNAL
PUBLICATION: ARCHIVES DE PEDIATRIE, 2002, V9, N2 (FEB), P130-135
GENUINE ARTICLE#: 529AG
PUBLISHER: EDITIONS SCIENTIFIQUES MEDICALES ELSEVIER, 23 RUE LINOIS, 75724 PARIS CEDEX 15, FRANCE
ISSN: 0929-693X
LANGUAGE: French DOCUMENT TYPE: ARTICLE

ABSTRACT: Aims. - To assess the frequency of acquisition of secondary *Helicobacter"** *pylori"** resistant-strains after a first course of antimicrobial treatment.

Patients and methods. - A retrospective study was performed during the 1994-2000 period, in 15 girls and eight boys, mean age 10.9 +/- 4.8 years (1.4-17 years), with *Helicobacter"** *pylori"** gastritis (culture and antimicrobial susceptibility) presenting a failure of first course treatment, with during one week a proton pump inhibitor and amoxicillin together with either clarithromycin (n=14) or metronidazole (n=9). Two endoscopies were performed, the first at the time of diagnosis and the second after the failure of bacterial eradication demonstrated by a positive C-13 urea breath test six weeks after the end of treatment. Antimicrobial susceptibility of all *Helicobacter"** *pylori"** strains was tested after each endoscopy and before starting a second course of the treatment.

Results. - Comparison of antimicrobial susceptibility before and after the first course of treatment showed that *Helicobacter"** *pylori"** strains were all sensitive to amoxicillin, clarithromycin-resistant in eight children (34.7%) before treatment vs 12 (52.1%) after treatment, p=0.42, ns, metronidazole-resistant in 13 (56.5%) vs 12 (52.1%), p=0.80,

ns, and both clarithromycin and metronidazole-resistant in four (17.3%) vs seven (30.4%), p=0.63, ns. Among the 14 children treated by a triple therapy including clarithromycin, three (21.4%) developed a secondary resistance to clarithromycin and in one metronidazole resistance was no more *detected"**. Among the nine children treated with a triple therapy including metronidazole, none developed a secondary resistance to metronidazole and one developed a secondary resistance to clarithromycin.

Conclusion. - This study shows the absence of amoxicillin-resistant strains, a high initial clarithromycin-resistant strains level (primary resistance), increasing after a first course of treatment, and for metronidazole a high initial level of resistance not influenced by treatment. Secondary clarithromycin-resistance of *Helicobacter"** *pylori"** strains following the first course of treatment could account for failure of bacterial eradication and suggests the importance of antimicrobial susceptibility. (C) 2002 Editions scientifiques et medicales Elsevier SAS.

15/3,AB/4 (Item 4 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

13560208 Document Delivery Available: 000174155500011 References: 10
TITLE: Increasing resistance of *Helicobacter"** *pylori"** to clarithromycin: Is the horse bolting?
AUTHOR(S): Grove DI (REPRINT); Koutsouridis G
AUTHOR(S) E-MAIL: david.grove@imvs.sa.gov.au
CORPORATE SOURCE: Queen Elizabeth Hosp, Dept Clin Microbiol & Infect Dis, /Woodville/SA 5001/Australia/ (REPRINT); Queen Elizabeth Hosp, Dept Clin Microbiol & Infect Dis, /Woodville/SA 5001/Australia/
PUBLICATION TYPE: JOURNAL
PUBLICATION: PATHOLOGY, 2002, V34, N1 (FEB), P71-73
GENUINE ARTICLE#: 526XQ
PUBLISHER: CARFAX PUBLISHING, RANKINE RD, BASINGSTOKE RG24 8PR, HANTS, ENGLAND
ISSN: 0031-3025
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: Aims: To *determine"** whether there has been a change in the patterns of susceptibility to various antibiotics of our isolates of *Helicobacter"** *pylori"** over a 5-year period from 1996 to 2000.

Methods: Five hundred and fourteen isolates of H. *pylori"** grown from gastric biopsies were tested for susceptibility to amoxycillin, clarithromycin, metronidazole and tetracycline. The usage of macrolide antibiotics in Australia was examined by calculating the numbers of prescriptions issued under the Australian pharmaceutical benefits scheme between 1992 and 2000.

Results: There were no changes in susceptibility of H. pylon to amoxycillin and tetracycline and there was a slight decline in resistance to metronidazole. In contrast, there was a step-wise 4-fold increase from 3.8 to 15.7% in the number of isolates resistant to clarithromycin and a similar increase in the mean minimum inhibitory concentration of clarithromycin during the 5-year period of observation. There was no change in overall macrolide consumption in Australia over this and the preceding 3 years. However, the pattern changed, with erythromycin usage being halved

and being replaced by roxithromycin and clarithromycin.

Conclusions: Resistance of H. *pylori"** to clarithromycin is increasing, possibly as a consequence of increased usage of roxithromycin and clarithromycin. More patients are likely to fail to respond to empirical therapy and will need microbiological investigation.

15/3,AB/5 (Item 5 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

13512715 Document Delivery Available: 000174003600001 References: 50
TITLE: Molecular testing for *antibiotic"** *resistance"** in *Helicobacter"** *pylori"**
AUTHOR(S): Owen RJ (REPRINT)
AUTHOR(S) E-MAIL: rowen@phls.nhs.uk
CORPORATE SOURCE: OHLS Cent Publ Hlth Lab, 61 Colindale Ave/London//England/ (REPRINT); OHLS Cent Publ Hlth Lab, /London//England/
PUBLICATION TYPE: JOURNAL
PUBLICATION: GUT, 2002, V50, N3 (MAR), P285-289
GENUINE ARTICLE#: 524FZ
PUBLISHER: BRITISH MED JOURNAL PUBL GROUP, BRITISH MED ASSOC HOUSE, TAVISTOCK SQUARE, LONDON WC1H 9JR, ENGLAND
ISSN: 0017-5749
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: An estimated 7.5 million individuals in England and Wales are actively infected with *Helicobacter"** *pylori"** and hence knowledge of local resistance rates is of growing importance. Also, information on strain resistance following treatment failure is crucial in selecting an appropriate regimen as the development of bacterial *resistance"** to *antibiotics"** makes retreatment difficult. Molecular test methods may have an impact on improving the availability and accuracy of information on H *pylori"** antimicrobial resistance to guide in the selection of primary as well as secondary backup treatment regimens.

15/3,AB/6 (Item 6 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

13474111 References: 34
TITLE: *Antibiotic"** *resistance"** of *Helicobacter"** *pylori"** strains in Japanese children
AUTHOR(S): Kato S (REPRINT); Fujimura S; Udagawa H; Shimizu T; Maisawa S; Ozawa K; Iinuma K
AUTHOR(S) E-MAIL: skato@ped.med.tohoku.ac.jp
CORPORATE SOURCE: Tohoku Univ, Aoba Ku, 1-1 Seiryo Machi/Sendai/Miyagi 9808574/Japan/ (REPRINT); Tohoku Univ, Aoba Ku, /Sendai/Miyagi 9808574/Japan/; Miyagi Univ, Dept Microbiol, /Miyagi//Japan/; Otsuka Tokyo Assay Labs, /Tokyo//Japan/; Juntendo Univ, Dept Pediat, /Tokyo 113//Japan/; Morioka Childrens Hosp, /Morioka/Iwate/Japan/
PUBLICATION TYPE: JOURNAL
PUBLICATION: JOURNAL OF CLINICAL MICROBIOLOGY, 2002, V40, N2 (FEB), P 649-653
GENUINE ARTICLE#: 519NG

PUBLISHER: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA
ISSN: 0095-1137
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: The resistance of *Helicobacter"** *pylori"** to the recently available antibiotic treatment regimens has been a growing problem. We investigated the prevalence of H. *pylori"** resistance to clarithromycin, metronidazole, and amoxicillin among 51 H. *pylori"** isolates from Japanese children. In addition, the *mutations"** of the corresponding gene were studied by PCR and restriction fragment length *polymorphism"** analysis. Primary resistance to clarithromycin, metronidazole, and amoxicillin was *detected"** in 29, 24, and 0% of strains, respectively. The eradication rates in clarithromycin-susceptible and -resistant strains were 89 and 56%, respectively ($P < 0.05$). The prevalence of strains with acquired resistance to clarithromycin (78%) was higher than that of strains with primary resistance ($P < 0.01$). Among the clarithromycin-resistant strains studied, 92% showed cross-resistance to azithromycin. No acquired resistance to amoxicillin was demonstrated. The A2144G *mutation"** in the *23S"** *rRNA"** gene was *detected"** in 11 of 12 (92%) clarithromycin-resistant strains tested, whereas the *mutation"** was not *detected"** in any of the 15 susceptible strains. The deletion of the rdxA gene was not demonstrated in any of the strains. The results indicate that a high prevalence of clarithromycin-resistant strains is associated with eradication failure. Testing of susceptibility to clarithromycin is recommended.

15/3,AB/7 (Item 7 from file: 440)

13260233 References: 82
TITLE: *Resistance"** of *Helicobacter"** *pylori"** to *antibiotics"** and its impact on treatment options
AUTHOR(S): Megraud F (REPRINT)
AUTHOR(S) E-MAIL: francis.megraud@chu-bordeaux.fr
CORPORATE SOURCE: Hop Pellegrin, Bacteriol Lab, Pl Amelie Raba Leon/F-33076 Bordeaux//France/ (REPRINT); Hop Pellegrin, Bacteriol Lab, /F-33076 Bordeaux//France/
PUBLICATION TYPE: JOURNAL
PUBLICATION: DRUG RESISTANCE UPDATES, 2001, V4, N3 (JUN), P178-186
GENUINE ARTICLE#: 494ZH
PUBLISHER: CHURCHILL LIVINGSTONE, JOURNAL PRODUCTION DEPT, ROBERT STEVENSON HOUSE, 1-3 BAXTERS PLACE, LEITH WALK, EDINBURGH EH1 3AF, MIDLOTHIAN, SCOTLAND
ISSN: 1368-7646
LANGUAGE: English DOCUMENT TYPE: REVIEW

ABSTRACT: The treatment of *Helicobacter"** *pylori"** infection is jeopardized by *resistance"** to the *antibiotics"** used, which turns out to be the main risk factor for failure. Resistance is due to point *mutations"**. For clarithromycin only two sites in the *23S"** *rRNA"** sequence are concerned and can be easily *detected"** by molecular methods, while for metronidazole several *mutations"** on rdxA and other genes can be responsible and so do not allow such *detection"**. The situation for the rare cases of amoxicillin resistance is not fully *determined"**. The impact of resistance on the clinical outcome is dramatic for clarithromycin

while it only decreases the success by 20% for metronidazole. (C) 2001 Harcourt Publishers Ltd.

15/3,AB/8 (Item 8 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

13239194 References: 33
TITLE: Rapid *detection"** of *mutations"** associated with resistance to erythromycin in Campylobacter jejuni/coli by PCR and line probe assay
AUTHOR(S): Niwa H; Chuma T; Okamoto K; Itoh K (REPRINT)
AUTHOR(S) E-MAIL: akikuji@mail.ecc.u-tokyo.ac.jp
CORPORATE SOURCE: Univ Tokyo, Bunkyo Ku, 1-1-1 Yayoi/Tokyo 1138657//Japan/ (REPRINT); Univ Tokyo, Bunkyo Ku, /Tokyo 1138657//Japan/; Kagoshima Univ, Lab Vet Publ Hlth, /Kagoshima 8900065//Japan/
PUBLICATION TYPE: JOURNAL
PUBLICATION: INTERNATIONAL JOURNAL OF ANTIMICROBIAL AGENTS, 2001, V18, N4 , P359-364
GENUINE ARTICLE#: 490WK
PUBLISHER: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS
ISSN: 0924-8579
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: *Mutation"** of 23S rDNA is one of the mechanisms of erythromycin resistance. PCR and line probe assay (PCR-LiPA) with ten oligonucleotide probes were developed to *detect"** the *mutations"** associated with macrolide resistance at positions of 2072, 2073 and 2074 in 23S rDNA of Campylobacter jejuni/coli. A2074 --> G *mutation"** was *detected"** in 12 of 25 isolates, which were resistant to erythromycin. No other *mutations"** in 23S rDNA were *detected"**. The rest of the strains were susceptible to erythromycin and no *mutation"** in 23S rDNA was *detected"**. Six laboratory induced erythromycin resistant *mutants"** had no *mutations"** in 23S rDNA. PCR-LiPA is a useful and rapid method to *detect"** *mutations"** in 23S rDNA associated with erythromycin resistance in C. jejuni/coli. (C) 2001 Elsevier Science B.V. and International Society of Chemotherapy, All rights reserved.

15/3,AB/9 (Item 9 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

13203897 References: 14
TITLE: Rapid and accurate *determination"** of genotypic clarithromycin resistance in cultured *Helicobacter"** *pylori"** by fluorescent in situ hybridization
AUTHOR(S): Russmann H (REPRINT); Adler K; Haas R; Gebert B; Koletzko S; Heesemann J
AUTHOR(S) E-MAIL: ruessmann@m3401.mpk.med.uni-muenchen.de
CORPORATE SOURCE: Univ Munich, Max von Pettenkofer Inst, Pettenkoferstr 9A/D-80336 Munich//Germany/ (REPRINT); Univ Munich, Max von Pettenkofer Inst Hyg & Med Mikrobiol, /D-80336 Munich//Germany/; Univ Munich, Dr v Haunersches Kinderspital, /D-80336 Munich//Germany/
PUBLICATION TYPE: JOURNAL
PUBLICATION: JOURNAL OF CLINICAL MICROBIOLOGY, 2001, V39, N11 (NOV), P 4142-4144
GENUINE ARTICLE#: 488KK

PUBLISHER: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA
ISSN: 0095-1137
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: Phenotypic susceptibility testing for clarithromycin by E-test and disk diffusion of 109 cultured *Helicobacter"** *pylori"** isolates was compared with the genotypic susceptibility *determination"** by fluorescent in situ hybridization (FISH). No discrepancies were found between these three methods. However, FISH has the advantage of providing results after 3 h.

15/3,AB/10 (Item 10 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

12897665 References: 22
TITLE: Prevalence and rapid identification of clarithromycin-resistant *Helicobacter"** *pylori"** isolates in children
AUTHOR(S): Yang YJ; Yang JC; Jeng YM; Chang MH; Ni YH (REPRINT)
AUTHOR(S) E-MAIL: yhni@ha.mc.ntu.edu.tw
CORPORATE SOURCE: Natl Taiwan Univ Hosp, Dept Pediat, 7 Chung Shan S Rd/Taipei 100//Taiwan/ (REPRINT); Natl Taiwan Univ, Dept Pediat, /Taipei 10764//Taiwan/; Natl Taiwan Univ, Dept Internal Med, /Taipei 10764//Taiwan/; Natl Taiwan Univ, Dept Pathol, /Taipei 10764//Taiwan/
PUBLICATION TYPE: JOURNAL
PUBLICATION: PEDIATRIC INFECTIOUS DISEASE JOURNAL, 2001, V20, N7 (JUL), P 662-666
GENUINE ARTICLE#: 452JV
PUBLISHER: LIPPINCOTT WILLIAMS & WILKINS, 530 WALNUT ST, PHILADELPHIA, PA 19106-3621 USA
ISSN: 0891-3668
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: Background. Little is known about the prevalence of *antibiotic"**-*resistant"** *Helicobacter"** *pylori"** infection in children. Culture and antimicrobial susceptibility testing are generally time-consuming and not a routine in many hospitals.

Objective. To investigate the prevalence of clarithromycin-resistant H. *pylori"** strains in children, to identify those isolates via rapid methodology and to examine the severity of gastritis caused by the *antibiotic"**-*resistant"** H. *pylori"** isolates.

Methods. Enrolled were 245 children investigated for H, *pylori"** infection by endoscopic examination. The gastric antral specimens were subjected to DNA extraction and polymerase chain reaction-restriction fragment length *polymorphism"** (PCR-RFLP) with primers specific to the H. *pylori"** *23S"** *rRNA"** gene. Conventional bacterial cultures were performed simultaneously as the diagnostic standard. Minimal inhibitory concentrations of clarithromycin and metronidazole were *determined"** by E test. This was used as a standard to *determine"** the sensitivity and specificity of the above PCR-RFLP assay. The specimens were processed for histologic examination and evaluated by the updated Sydney system.

Results. H. *pylori"** was isolated in 67 of the 245 children; 12 (18%) of them were clarithromycin-resistant and 6 (9%) were

metronidazole-resistant. No difference in histologic examinations was noted between the *antibiotic"**-*resistant"** and -susceptible strains. We performed PCR-RFLP with all 12 clarithromycin-resistant isolates: 10 had a *23S"** *ribosomal"** *RNA"** A2144G point *mutation"**; 1 had a mixture of an A2143G point *mutant"** and susceptible strains; and 1 had neither of the 2 *mutations"**.

Conclusions. The prevalence of clarithromycin-resistant H. *pylori"** isolates in Taiwanese children is 18%. PCR-RFLP had a high sensitivity (92%) and specificity (100%) for the clarithromycin resistance gene *mutation"** *determination"**. The dominant *mutation"** is A2144G. PCR-RFLP provides a rapid and accurate approach to *detect"** clarithromycin-resistant strains within 24 h.

15/3,AB/11 (Item 11 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

12589226 References: 36
TITLE: Molecular resistance testing of *Helicobacter"** *pylori"** in gastric biopsies
AUTHOR(S): Pena JA; Fox JG; Ferraro MJ; Versalovic J (REPRINT)
AUTHOR(S) E-MAIL: jversalovic@partners.org
CORPORATE SOURCE: Massachusetts Gen Hosp, Div Lab Med, GRJ 529,55 Fruit St/Boston//MA/02114 (REPRINT); Massachusetts Gen Hosp, Div Lab Med, /Boston//MA/02114; Northeastern Univ, Dept Med Lab Sci, /Boston//MA/02115 ; MIT, Div Comparat Med, /Cambridge//MA/02139; Harvard Univ, Dept Pathol, /Boston//MA/02115
PUBLICATION TYPE: JOURNAL
PUBLICATION: ARCHIVES OF PATHOLOGY & LABORATORY MEDICINE, 2001, V125, N4 (APR), P493-497
GENUINE ARTICLE#: 419ZY
PUBLISHER: COLLEGE AMER PATHOLOGISTS, C/O KIMBERLY GACKI, 325 WAUKEGAN RD, NORTHFIELD, IL 60093-2750 USA
ISSN: 0003-9985
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: Objective.-To evaluate simultaneous diagnosis of infection and molecular resistance testing of *Helicobacter"** *pylori"**.

Methods.-Gastric biopsies were obtained from 26 rapid urease-positive and 51 rapid urease-negative test kits used to diagnose H *pylori"** infection. Following glass bead-assisted DNA isolation, amplification of H *pylori"** 16S ribosomal DNA (rDNA), glmM, and 23S rDNA target genes was performed.

Results.-*Helicobacter"** *pylori"** DNA was successfully amplified from 100% (26/26) of urease-positive and 3.9% (2/ 51) of urease-negative gastric biopsies. Subsequent restriction enzyme-mediated digestion of 23S rDNA amplification products revealed that 17% (4/24) of urease-positive and H *pylori"** DNA-positive biopsy specimens contained point *mutations"** (A2142G or A2143G) associated with clarithromycin resistance. *Helicobacter"** *pylori"** DNA from gastric biopsies was successfully amplified 8 weeks following rapid urease testing.

Conclusion.-*Helicobacter"** *pylori"** genotyping may be used to *detect"** macrolide-resistant H *pylori"** in individuals prior to initiation of therapy or in patients refractory to anti-H *pylori"**

therapy. Two urease-negative specimens yielded *Helicobacter"** DNA distinct from that of H *pylori"** and indicated the need for further investigations of *Helicobacter"** species present in the human stomach.

15/3,AB/12 (Item 12 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

12455273 References: 28
TITLE: Spontaneous *mutations"** that confer *antibiotic"** *resistance"** in *Helicobacter"** *pylori"**
AUTHOR(S): Wang GE; Wilson TJM; Jiang Q; Taylor DE (REPRINT)
AUTHOR(S) E-MAIL: diane.taylor@ualberta.ca
CORPORATE SOURCE: Univ Alberta, Dept Med Microbiol & Immunol, /Edmonton/AB T6G 2H7/Canada/ (REPRINT); Univ Alberta, Dept Med Microbiol & Immunol, /Edmonton/AB T6G 2H7/Canada/
PUBLICATION TYPE: JOURNAL
PUBLICATION: ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, 2001, V45, N3 (MAR), P 727-733
GENUINE ARTICLE#: 405AJ
PUBLISHER: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA
ISSN: 0066-4804
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: In this study, we systematically examined in vitro frequencies and spectra of the spontaneous *mutations"** in *Helicobacter"** *pylori"** that confer resistance to clarithromycin (Cla(r)), metronidazole (Mtz(r)), amoxicillin (Amx(r)), ciprofloxacin (Cip(r)), and rifampin (Rif(r)), The *mutation"** rate of Rif(r) or Cip(r) *determined"** in a fluctuation assay is 1 x 10(-8) to 2 x 10(-8) per cell per division, In contrast, the *mutation"** rates of Cla(r), Mtz(r), and Amx(r) are much lower (< 10(-9)). However, Mtz(r) *mutants"** could be readily selected in vitro by using the serial passage method, suggesting that the *mutagenic"** effect and selective effect of a sublethal dose of metronidazole contribute to the rapid development of Mtz(r). Analysis of spontaneous Rif(r), Cla(r), and Cip(r) *mutants"** confirmed previous results indicating that *mutations"** within the rpoB gene, the *23S"** *rRNA"** gene, and the gyrA gene, respectively, are responsible; also, several new *mutant"** alleles were identified. Mtz(r) *mutants"** resulted most frequently, but not always, from *mutations"** in the rdxA gene. DNA fragments containing each *mutant"** allele could readily transform susceptible H. *pylori"** strains to resistance, confirming that each *mutant"** allele is responsible for the resistance phenotype.

15/3,AB/13 (Item 13 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

12339143 References: 26
TITLE: Comparison of fluorescent in situ hybridization and conventional culturing for *detection"** of *Helicobacter"** *pylori"** in gastric biopsy specimens
AUTHOR(S): Russmann H (REPRINT); Kempf VAJ; Koletzko S; Heesemann J; Autenrieth IB
AUTHOR(S) E-MAIL: ruessmann@m3401.mpk.med.uni-muenchen.de

CORPORATE SOURCE: Univ Munich, Max von Pettenkofer Inst Hyg & Med Mikrobiol, Pettenkoferstr 9A/D-80336 Munich//Germany/ (REPRINT); Univ Munich, Max von Pettenkofer Inst Hyg & Med Mikrobiol, /D-80336 Munich//Germany/; Univ Munich, Dr v Haunersches Kinderspital, /D-80336 Munich//Germany/; Univ Klinikum Tubingen, Inst Med Mikrobiol, /D-72076 Tubingen//Germany/
PUBLICATION TYPE: JOURNAL
PUBLICATION: JOURNAL OF CLINICAL MICROBIOLOGY, 2001, V39, N1 (JAN), P 304-308
GENUINE ARTICLE#: 393KZ
PUBLISHER: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA
ISSN: 0095-1137
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: In this study, we have investigated 201 gastric biopsy specimens obtained from dyspeptic patients for the presence of *Helicobacter"** *pylori"**, By means of fluorescent in situ hybridization (FISH) with rRNA-targeted fluorescence-labeled oligonucleotide probes specific for H. *pylori"**, this pathogen was *detected"** in 63 biopsy specimens. By using conventional culturing, H. *pylori"** was isolated from 49 of these 63 gastric biopsy specimens. In contrast, FISH failed to identify H. *pylori"** in four samples from which the pathogen was cultured, The lowest sensitivity was obtained by using the urease test. H. *pylori"** was *detected"** indirectly by this method in 43 of 67 biopsy specimens, which were positive for the pathogen as *determined"** by FISH and/or culturing. All 49 H. *pylori"** isolates that were *detected"** by FISH and culturing underwent antimicrobial susceptibility testing for clarithromycin, a macrolide drug that is a key component in the therapy of peptic ulcer disease caused by this pathogen, Clarithromycin susceptibility testing of cultured isolates was carried out by the E-test, whereas FISH was used on biopsy specimens to *detect"** clarithromycin-resistant *mutant"** strains. No discrepancies were found between these two methods. Thirty-seven strains were clarithromycin sensitive, and eight H. *pylori"** isolates were resistant to the macrolide. From another four biopsy specimens, a mixture of clarithromycin-sensitive and -resistant strains was identified by both methods. Thus, FISH is a reliable technique for *determining"** the clarithromycin susceptibility of this pathogen, Taken together, FISH is a more sensitive and rapid technique than culturing for *detection"** of H. *pylori"** in gastric biopsy specimens. However, in the microbiology routine diagnostic laboratory, the combination of both FISH and conventional culturing significantly increases the sensitivity in *detection"** of H. *pylori"**.

12265257 References: 31
TITLE: *Mutation"** in *23S"** *rRNA"** responsible for resistance to 16-membered macrolides and streptogramins in Streptococcus pneumoniae
AUTHOR(S): Depardieu F (REPRINT); Courvalin P
AUTHOR(S) E-MAIL: fdepard@pasteur.fr
CORPORATE SOURCE: Inst Pasteur, Unite Agents Antibacteriens, 25 Rue Docteur Roux/F-75724 Paris 15//France/ (REPRINT); Inst Pasteur, Unite Agents Antibacteriens, /F-75724 Paris 15//France/
PUBLICATION TYPE: JOURNAL

PUBLICATION: ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, 2001, V45, N1 (JAN), P 319-323
GENUINE ARTICLE#: 384NV
PUBLISHER: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA
ISSN: 0066-4804
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: Streptococcus pneumoniae clinical isolate BM4455 was resistant to 16-membered macrolides and to streptogramins. This unusual resistance phenotype was due to an A(2062)C (Escherichia coli numbering) *mutation"** in domain V of the four copies of *23S"** *rRNA"**.

15/3,AB/15 (Item 15 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

12068153 References: 41
TITLE: Antimicrobial susceptibility testing for *Helicobacter"** *pylori"** : Sensitivity test results and their clinical relevance
AUTHOR(S): Osato MS (REPRINT)
AUTHOR(S) E-MAIL: mosato@bcm.tmc.edu
CORPORATE SOURCE: Vet Affairs Med Ctr, Gastroenterol Microbiol Lab, 2002 Holcombe Blvd,Rm 3A-320/Houston//TX/77030 (REPRINT); Vet Affairs Med Ctr, Gastroenterol Microbiol Lab, /Houston//TX/77030; Baylor Coll Med, /Houston//TX/77030
PUBLICATION TYPE: JOURNAL
PUBLICATION: CURRENT PHARMACEUTICAL DESIGN, 2000, V6, N15 (OCT), P1545-1555
GENUINE ARTICLE#: 363MA
PUBLISHER: BENTHAM SCIENCE PUBL LTD, PO BOX 1673, 1200 BR HILVERSUM, NETHERLANDS
ISSN: 1381-6128
LANGUAGE: English DOCUMENT TYPE: REVIEW

ABSTRACT: There are multiple test methodologies to *determine"** the antibiogram of an organism. Standardized susceptibility test methods are based upon rapidly growing, aerobic microorganisms in which overnight incubation results in definitive endpoints. In vitro susceptibility testing for fastidious organisms that require complex media for growth, require incubation in atmospheres other than ambient air, or are slow-growing (anaerobes, mycobacteria, filamentous fungi) are problematic and in general are not standardized. H. *pylori"** falls into this category of troublesome organisms. For the microaerobic organism H. *pylori"**, testing is challenging because the organism grows slowly even under optimal culture conditions. Recently the National Committee for Clinical Laboratory Standards (NCCLS) approved the agar dilution method as the test of choice for testing H. *pylori"**. While not entirely reliable in predicting the outcome of treatment for metronidazole resistant organisms, the resistance *determined"** for clarithromycin by this method generally predicts treatment failure. Quality control breakpoints for H. *pylori"** ATCC 43504 were established and breakpoints for clarithromycin were approved by the NCCLS in 1999. Breakpoints are minimum inhibitory concentrations (MIC) of a drug at which an organism is deemed either susceptible or *resistant"** to the *antibiotic"** using standard dosing regimens containing that drug. Significant progress has been made with respect to development of tests to *detect"** antimicrobial resistance, but there still. remains no consensus as to the breakpoints for agents used in the treatment of H. *pylori"**

infection other than clarithromycin. This article will address the controversies associated with the reporting of *antibiotic"** *resistance"** data and the interpretation of these data.

15/3,AB/16 (Item 16 from file: 440)

11748280 References: 33
TITLE: High prevalence of *Helicobacter"** *pylori"** infection with dual resistance to metronidazole and clarithromycin in Hong Kong
AUTHOR(S): Wang WH; Wong BCY (REPRINT); Mukhopadhyay AK; Berg DE; Cho CH; Lai KC; Hu WHC; Fung FMY; Hui WM; Lam SK
AUTHOR(S) E-MAIL: bcywong@hku.hk
CORPORATE SOURCE: Univ Hong Kong, Dept Med, /Hong Kong/Hong Kong/Peoples R China/ (REPRINT); Univ Hong Kong, Dept Med, /Hong Kong/Hong Kong/Peoples R China/; Univ Hong Kong, Dept Pharmacol, /Hong Kong/Hong Kong/Peoples R China/; Washington Univ, Dept Mol Microbiol, /St Louis//MO/63110
PUBLICATION TYPE: JOURNAL
PUBLICATION: ALIMENTARY PHARMACOLOGY & THERAPEUTICS, 2000, V14, N7 (JUL), P 901-910
GENUINE ARTICLE#: 328GR
PUBLISHER: BLACKWELL SCIENCE LTD, P O BOX 88, OSNEY MEAD, OXFORD OX2 0NE, OXON, ENGLAND
ISSN: 0269-2813
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: Background: Metronidazole resistance is a common problem in most Asian countries, and clarithromycin has been widely used in Hong Kong.

Aim: To *determine"** the prevalence of *Helicobacter"** *pylori"** strains resistant to metronidazole and clarithromycin in Hong Kong and to assess the effect on eradication rates. Also to *determine"** the genetic *mutation"** in relation to phenotypic divergence in clarithromycin-resistant strains.

Methods: H. *pylori"** were cultured from gastric biopsies obtained from 87 patients during upper endoscopy. Minimal inhibitory concentrations of metronidazole and clarithromycin were *determined"** by Etest and agar dilution methods. *Mutations"** in clarithromycin-resistant strains were identified by polymerase chain reaction and restriction analysis. Random amplified *polymorphic"** DNA fingerprinting was performed on clarithromycin-resistant and susceptible isolates.

Results: The prevalences of H. *pylori"** strains resistant to metronidazole and clarithromycin were 49.4% and 10.8%, respectively, in Hong Kong. Dual resistance to metronidazole and clarithromycin were found in 7.2% of patients. The agreement between E-test and agar dilution methods was *determined"** by error-rate bound analysis as 95.4% for metronidazole and 100% for clarithromycin. Dual resistant strains reduced the eradication rate to 66.7%. Among clarithromycin-resistant strains tested, all were due to A2144G point *mutation"** in *23S"** *rRNA"** gene. Random amplified *polymorphic"** DNA fingerprinting suggested various phenotypically mixed populations.

Conclusions: The prevalence of metronidazole-resistant H. *pylori"** strains remained static whilst the prevalence of clarithromycin-resistant strains was not rare in Hong Kong. An alarming 7.2% of patients were

resistant to both the antimicrobials, which had a definite impact on treatment success. All cases of resistance to clarithromycin were due to A2144G *mutation"** in *23S"** *rRNA"** of H. *pylori"**.

15/3,AB/17 (Item 17 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

11583303 References: 27
TITLE: Rapid and specific *detection"** of *Helicobacter"** *pylori"** macrolide resistance in gastric tissue by fluorescent in situ hybridisation
AUTHOR(S): Trebesius K; Panthel K; Strobel S; Vogt K; Faller G; Kirchner T; Kist M; Heesemann J; Haas R (REPRINT)
AUTHOR(S) E-MAIL: haas@m3401.mpk.med.uni-muenchen.de
CORPORATE SOURCE: Univ Munich, Max Von Pettenkofer Inst Hyg & Med Microbiol, Pettenkoferstr 9A/D-80336 Munich//Germany/ (REPRINT); Univ Munich, Max Von Pettenkofer Inst Hyg & Med Microbiol, /D-80336 Munich//Germany/; Univ Freiburg, Inst Med Microbiol & Hyg, /D-7800 Freiburg//Germany/; Humboldt Univ, Dept Microbiol, /Berlin//Germany/; Humboldt Univ, Charite, /Berlin//Germany/; Univ Erlangen Nurnberg, Inst Pathol, /D-8520 Erlangen//Germany/
PUBLICATION TYPE: JOURNAL
PUBLICATION: GUT, 2000, V46, N5 (MAY), P608-614
GENUINE ARTICLE#: 308HQ
PUBLISHER: BRITISH MED JOURNAL PUBL GROUP, BRITISH MED ASSOC HOUSE, TAVISTOCK SQUARE, LONDON WC1H 9JR, ENGLAND
ISSN: 0017-5749
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: Background-The development of macrolide resistance in *Helicobacter"** *pylori"** is considered an essential reason for failure of antibiotic eradication therapies. The predominant mechanism of resistance to macrolides, particularly clarithromycin, is based on three defined *mutations"** within *23S"** *rRNA"**, resulting in decreased binding of the antibiotic to the bacterial ribosome.

Aim-To develop an rRNA based whole cell hybridisation method to *detect"** *Helicobacter"** species in situ within gastric tissue, simultaneously with its clarithromycin resistance genotype.

Methods-A set of fluorescent labelled oligonucleotide probes was developed, binding either to H *pylori"** 16S *rRNA"** or *23S"** *rRNA"** sequences containing specific point *mutations"** responsible for clarithromycin resistance. After hybridisation and stringent washing procedures, labelling of intact single bacteria was monitored by fluorescence microscopy. The new approach was compared with PCR based assays, histology, and microbiological culture.

Results-In comparison with the phenotypic resistance measurement by E test, the genotypic clarithromycin resistance correlated perfectly (100%) for 35 H *pylori"** isolates analysed. In a set of gastric biopsy specimens (27) H *pylori"** infection was confirmed by histology (17/27) and correctly *detected"** by whole cell hybridisation. Five clarithromycin resistant strains were identified in gastric tissue specimens directly. Furthermore, non-cultivable coccoid forms of H *pylori"** were easily *detectable"** by whole cell hybridisation.

Conclusions-Whole cell hybridisation of rRNA holds great promise for cultivation independent, reliable, and rapid (three hours) genotypic *determination"** of clarithromycin resistance in H *pylori"**. Compared with PCR techniques it is independent of nucleic acid preparations, not prone to inhibition, and allows semiquantitative visualisation of the bacteria within intact tissue samples.

15/3,AB/18 (Item 18 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

10974665 References: 71
TITLE: The role of PCR in the diagnosis of *Helicobacter"** *pylori"** infections
AUTHOR(S): Kabir S (REPRINT)
CORPORATE SOURCE: Acad Res & Informat Management, Tobaksspinnargatan 5/S-11736 Stockholm//Sweden/ (REPRINT); Acad Res & Informat Management, /S-11736 Stockholm//Sweden/
PUBLICATION TYPE: JOURNAL
PUBLICATION: REVIEWS IN MEDICAL MICROBIOLOGY, 1999, V10, N4 (OCT), P197-212
GENUINE ARTICLE#: 242AA
PUBLISHER: LIPPINCOTT WILLIAMS & WILKINS, 227 EAST WASHINGTON SQ, PHILADELPHIA, PA 19106 USA
ISSN: 0954-139X
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: PCR, a powerful method known for its high sensitivity, has been used in the diagnosis of *Helicobacter"** *pylori"** infections. Several PCR protocols, differing from each other mostly in the choice of primers, have been developed to *detect"** the organism in a range of clinical specimens such as gastric biopsy, gastric juice, stool, saliva and dental plaque. Various genomic targets have been used in these protocols, such as the urease A gene (ureA), the urease C gene (ureC), the 16S rRNA gene, a randomly selected sequence of chromosomal DNA, the 26-kDa species-specific antigen gene and the 0.86-kb gene of H. *pylori"**. Although PCR of these targets displayed high sensitivity and specificity, its advantage over other diagnostic methods was not obvious when using gastric biopsy specimens. Because of its high sensitivity, PCR can be useful to *detect"** low numbers of organisms present in specimens such as gastric juice, saliva and faeces, and for the post-treatment diagnosis of H. *pylori"** when the bacterial load may be very low. PCR-based fingerprinting techniques such as restriction fragment length *polymorphism"** analysis and the randomly amplified *polymorphic"** DNA method are useful in the post-treatment period in differentiating between strains. Also, PCR has been used to *detect"** *antibiotic"** (clarithromycin) *resistance"** in H. *pylori"**. Because of its high sensitivity, PCR carries a high risk of contamination leading to false-positive results. It is technically demanding and not generally available as a routine diagnostic tool. However, PCR does not have any specific requirement for transportation of the specimens and the results can be obtained in a short period of time.

15/3,AB/19 (Item 19 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

10962546 References: 23
TITLE: Simultaneous colonisation of *Helicobacter"** *pylori"** with and without *mutations"** in the *23S"** *rRNA"** gene in patients with no history of clarithromycin exposure
AUTHOR(S): Matsuoka M (REPRINT); Yoshida Y; Hayakawa K; Fukuchi S; Sugano K
CORPORATE SOURCE: Mishuku Hosp, Meguro Ku, 5-33-12 Kamimeguro/Tokyo 153//Japan/ (REPRINT); Mishuku Hosp, Meguro Ku, /Tokyo 153//Japan/; Univ Tokyo, Meguro Ku, /Tokyo//Japan/
PUBLICATION TYPE: JOURNAL
PUBLICATION: GUT, 1999, V45, N4 (OCT), P503-507
GENUINE ARTICLE#: 239XA
PUBLISHER: BRITISH MED JOURNAL PUBL GROUP, BRITISH MED ASSOC HOUSE, TAVISTOCK SQUARE, LONDON WC1H 9JR, ENGLAND
ISSN: 0017-5749
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: Background-It was recently reported that A to G transition *mutations"** at positions 2143 and 2144 in the *23S"** *rRNA"** gene are associated with clarithromycin resistance in *Helicobacter"** *pylori"**.

Aims-To study the incidence and mechanism of development of clarithromycin resistance by analysing these *mutations"**.

Subjects-Eighty two H *pylori"** positive patients who had an endoscopic examination and no history of treatment with macrolide *antibiotics"**.

Methods-Clarithromycin *resistance"** was *screened"** for by polymerase chain reaction-restriction fragment length *polymorphism"** of the *23S"** *rRNA"** gene coupled with antibiotic susceptibility testing. In clinical isolates with *mutations"** or resistance, *mutations"** in individual colonies were analysed by direct sequencing.

Results-Of the 79 amplicons (DNA fragments amplified by polymerase chain reaction), Alw26I and MboII digestion disclosed the *mutation"** in four (5%) and one (1%) respectively. However, the Alw26I cleavage was incomplete in two of the four amplicons, as was the MboII cleavage. Individual colony analysis of the isolates with incomplete cleavage patterns showed the presence of both wild type and *mutated"** strains in the *23S"** *rRNA"** genes.

Conclusions-Both clarithromycin sensitive and resistant strains colonised in some patients with no history of exposure to macrolides. The results suggest that resistant strains may not be formed but selected by clarithromycin administration.

15/3,AB/20 (Item 20 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

10744791 References: 36
TITLE: Effect of clarithromycin and omeprazole therapy on the diversity and stability of genotypes of *Helicobacter"** *pylori"** from duodenal ulcer patients
AUTHOR(S): Owen RJ (REPRINT); Slater ER; Gibson J; Lorenz E; Tompkins DS
CORPORATE SOURCE: Cent Publ Hlth Lab, Helicobacter Reference Unit, 61

Colindale Ave/London NW9 5HT//England/ (REPRINT); Cent Publ Hlth Lab, Helicobacter Reference Unit, /London NW9 5HT//England/; Publ Hlth Lab, /Leeds/W Yorkshire/England/
PUBLICATION TYPE: JOURNAL
PUBLICATION: MICROBIAL DRUG RESISTANCE-MECHANISMS EPIDEMIOLOGY AND DISEASE , 1999, V5, N2 (SUM), P141-146
GENUINE ARTICLE#: 216DG
PUBLISHER: MARY ANN LIEBERT INC PUBL, 2 MADISON AVENUE, LARCHMONT, NY 10538 USA
ISSN: 1076-6294
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: The genotypes of multiple isolates of *Helicobacter"** *pylori"** from 17 duodenal ulcer patients in the United Kingdom were compared to *determine"** reasons for treatment failure, Isolates were from antrum and corpus biopsies taken before and after dual therapy with clarithromycin and omeprazole, All isolates were tested for *antibiotic"** *resistance"** and characterised by a novel scheme combining polymerase chain reaction-restriction fragment length *polymorphism"** (PCR-RFLP) analysis of the ureA + ureB and *23S"** *rRNA"** genes, vacA signal and midregion genotypes, and PCR *detection"** of cagA, Combined genotypes of paired pre- and post-treatment isolates from 8 patients showed an infection with a single strain of H. *pylori"** that had acquired resistance to clarithromycin. In 4 other patients, acquisition of clarithromycin resistance was associated with the presence of different strain types of H, *pylori"**, The remaining 5 patients had clarithromycin-sensitive isolates. Overall, H, *pylori"** from different patients had diverse genotypes, yet most (70%) were colonized by the same predominant and stable strain in both the antrum and corpus, There was no link between the emergence of in vitro clarithromycin resistance and a particular strain genotype for these UK isolates. It was concluded that colonization with a clarithromycin-resistant H, *pylori"** was due to selection of a resistant strain or clonal variant within the infecting population, Present genomic markers had low predictive value for emergence of resistance.

15/3,AB/21 (Item 21 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

10088299 References: 24
TITLE: Microbiological aspects of *antibiotic"** *resistant"** *Helicobacter"** *pylori"** strains
AUTHOR(S): Monteiro L; Megraud F (REPRINT)
CORPORATE SOURCE: CHU Bordeaux, Lab Bacteriol Enfants, Pl Amelie Raba Leon/F-33076 Bordeaux//France/ (REPRINT); Pellegrin Hosp, Lab Bacteriol, /Bordeaux//France/
PUBLICATION TYPE: JOURNAL
PUBLICATION: ITALIAN JOURNAL OF GASTROENTEROLOGY AND HEPATOLOGY, 1998, V30 , ,3 (OCT), PS329-S333
GENUINE ARTICLE#: 146WH
PUBLISHER: PACINI EDITORE, VIA DELLA GHERARDESCA-ZONA INDUSTRIALE, 56014 OSPEDALETTO PISA, ITALY
ISSN: 1125-8055
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: *Resistance"** of *Helicobacter"** *pylori"** to *antibiotics"** has been described for macrolides, nitroimidizoles, and fluoroquinolones.

In 1996, the mechanism of resistance to macrolides was *determined"** to be a point *mutation"** on the *23S"** *rRNA"** which leads to decreased binding of macrolides to the ribosome. Recently, *mutations"** in the gene coding for nitroreductase have been linked to resistance to nitroimidazoles but more work will be necessary to *determine"** whether this is the only mechanism involved. Point *mutations"** have also been associated with resistance to fluro-quinolones. A decreased susceptibility to amoxicillin has been observed and may be linked to changes in the penicillin binding proteins. The same phenotypic methods generally used to rest antibiotic susceptibility can be applied to *Helicobacter"** *pylori"**. The disk diffusion method can be used for macrolides, the E-test for amoxicillin, and the point limit method for nitroimidazoles but the reference method of all of these is the agar dilution method. Molecular methods such as polymerase chain reaction E-RFLP and various techniques using hybridization can also be employed but to date they have only been used for macrolides. These techniques have the advantage that they can be applied directly to the biopsy specimen.

15/3,AB/22 (Item 22 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

09775593 References: 19
TITLE: Co-*detection"** of *Helicobacter"** *pylori"** and of its resistance to clarithromycin by PCR
AUTHOR(S): Sevin E; Lamarque D; Delchier JC; Soussy CJ; Tankovic J (REPRINT)
CORPORATE SOURCE: HOP HENRI MONDOR,SERV BACTERIOL VIROL HYG/CRETEIL//FRANCE/ (REPRINT); HOP HENRI MONDOR,SERV BACTERIOL VIROL HYG/CRETEIL//FRANCE/; HOP HENRI MONDOR,SERV HEPATOGASTROENTEROL/CRETEIL//FRANCE/
PUBLICATION TYPE: JOURNAL
PUBLICATION: FEMS MICROBIOLOGY LETTERS, 1998, V165, N2 (AUG 15), P369-372
GENUINE ARTICLE#: 112TG
PUBLISHER: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS
ISSN: 0378-1097
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: Our aim was to develop a rapid molecular test based on polymerase chain reaction-restriction fragment length *polymorphism"** (PCR-RFLP) and making it possible to *detect"** *Helicobacter"** *pylori"** directly from gastric biopsy samples, and to test its susceptibility to clarithromycin. A 629-bp fragment of the *23S"** *rRNA"** gene of H. *pylori"** H. was amplified by PCR and the *mutations"** responsible for clarithromycin resistance were *detected"** with BsaI and BbsI restriction endonucleases. Thirty-five gastric samples were tested in parallel by standard microbiologic methods (culture and clarithromycin susceptibility testing with E-test strips) and by PCR-RFLP. The 10 culture-negative samples were also PCR-negative. Sixteen out of the 25 culture positive samples (64%) were PCR-positive. RFLP analysis could be done in 12 cases and the results were in agreement with those of the E-test: susceptibility in five cases, resistance in seven (six A2144G *mutations"** and one A2143G *mutation"**).

15/3,AB/23 (Item 23 from file: 440)

DIALOG(R)File 440:Current Contents Search(R)

09023243 References: 25
TITLE: *Helicobacter"** *pylori"** *resistance"** to *antibiotics"**
AUTHOR(S): Megraud F (REPRINT)
CORPORATE SOURCE: HOP PELLEGRIN,CTR NATL REFERENCE CAMPYLOBACTERS & HELICOBACTERS, BACTERIOL LAB/F-33076 BORDEAUX//FRANCE/ (REPRINT)
PUBLICATION TYPE: JOURNAL
PUBLICATION: PRESSE MEDICALE, 1997, V26, N37 (NOV 29), P1775-1780
GENUINE ARTICLE#: YK113
PUBLISHER: MASSON EDITEUR, 120 BLVD SAINT-GERMAIN, 75280 PARIS 06, FRANCE
ISSN: 0755-4982
LANGUAGE: French DOCUMENT TYPE: REVIEW

ABSTRACT: Eradication: Due to its causal role, eradication of Heiicobacter *pylori"** has become an essential part of therapy for many gastroduodenal diseases. Treatment is based on antibiotics as for any infectious disease. Generally two antibiotics, clarithromycin and amoxicillin or metronidazole and an antisecretory agent are combined in a 7-day regimen.

Development of resistance: The main cause of treatment failure is acquired H. *pylori"** resistance to clarithromycin and/or metronidazole. Macrolide resistance results from defective ribosome binding and is associated with a point *mutation"** on the gene encoding for the *23S"** *ribosomal"** *RNA"**. Strong resistance is acquired. Nitroimidazole resistance appears to result form the incapacity of H. *pylori"** to reduce the nitrate moiety necessary for toxicity. There is a minimum inhibitory concentration gradient. Epidemiological data show that the rate of primary resistance in France is about 10% for clarithromycine and 30% for metronidazole, a rate which would allow use without susceptibility resting for every case. Good compliance is the key to avoiding development of resistance during treatment.

In case of treatment failure: Susceptibilty tests are required before attempting a second eradication after initial failure. Though difficult, culture of the H. *pylori"** strain is required to *determine"** the most effective antibacterial agent. In case of nitroimidazole resistance, amoxicillin can be used with clarithromycin and a proton pump inhibitor and metronidazole in case of clarithromycin resistance with amoxicillin and proton pump inhibitor treatment Combination regimens using ranitidine instead of a proton pump inhibitor should be given for 14 days instead of 7. If *resistance"** to both *antibiotics"** is observed, the amoxicillin-metronidazole-proton inhibitor combination for 10 days at a higher dose of metronidazole (500 mg t.i.d.) is recommended. Trials with other compounds are required for such difficult cases. (C) 1997, Masson, Paris.

15/3,AB/24 (Item 24 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

09020464 References: 35
TITLE: Macrolide resistance in *Helicobacter"** *pylori"**: Rapid *detection"** of point *mutations"** and assays of macrolide binding to ribosomes
AUTHOR(S): Occhialini A; Urdaci M; DoucetPopulaire F; Bebear CM;

Lamouliatte H; Megraud F (REPRINT)
CORPORATE SOURCE: HOP PELLEGRIN,BACTERIOL LAB, PL AMELIE RABA LEON/F-33076 BORDEAUX//FRANCE/ (REPRINT); HOP PELLEGRIN,BACTERIOL LAB/F-33076 BORDEAUX//FRANCE/; UNIV BORDEAUX 2,/F-33076 BORDEAUX//FRANCE/; HOP ST ANDRE,/BORDEAUX//FRANCE/; ECOLE NATL INGENIEURS TRAVAUX AGR,MICROBIOL LAB/GRADIGNAN//FRANCE/; CHU PITIE SALPETRIERE,/PARIS//FRANCE/; HOP MIGNOT,/LE CHESNAY//FRANCE/
PUBLICATION TYPE: JOURNAL
PUBLICATION: ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, 1997, V41, N12 (DEC), P 2724-2728
GENUINE ARTICLE#: YK234
PUBLISHER: AMER SOC MICROBIOLOGY, 1325 MASSACHUSETTS AVENUE, NW, WASHINGTON, DC 20005-4171
ISSN: 0066-4804
LANGUAGE: English DOCUMENT TYPE: ARTICLE
ABSTRACT: Resistance of *Helicobacter"** *pylori"** to macrolides is a major cause of failure of eradication therapies. Single base substitutions in the H. *pylori"** *23S"** *rRNA"** genes have been associated with macrolide resistance in the United States, Our goal was to extend this work to European strains, to *determine"** the consequence of this *mutation"** on erythromycin binding to H. *pylori"** ribosomes, and to find a quick method to *detect"** the *mutation"**, Seven pairs of H. *pylori"** strains were used, the parent strain being naturally susceptible to macrolides and the second strain having acquired an in vivo resistance during a treatment regimen that included clarithromycin. The identity of the strains was confirmed by random amplified *polymorphic"** DNA testing with two different primers, indicating that resistance was the result of the selection of variants of the infecting strain, All resistant strains were found to have point *mutations"** at position 2143 (three cases) or 2144 (four cases) but never on the opposite DNA fragment of domain V of the *23S"** *rRNA"** gene. The *mutation"** was A-->G in all cases except one (A-->C) at position 2143. Using BsaI and BbsI restriction enzymes on the amplified products, we confirmed the *mutations"** of A-->G at positions 2144 and 2143, respectively, Macrolide binding was tested on purified ribosomes isolated from four pairs of strains with [C-14]erythromycin. Erythromycin binding increased in a dose-dependent manner for the susceptible strain but not for the resistant one. In conclusion we suggest that the limited disruption of the peptidyltransferase loop conformation, caused by a point *mutation"**, reduces drug binding and consequently confers resistance to macrolides. Finally, the macrolide resistance could be *detected"** without sequencing by performing restriction fragment length *polymorphism"** with appropriate restriction enzymes.

15/3,AB/25 (Item 25 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

08428578 References: 39
TITLE: *Resistance"** of *Helicobacter"** *pylori"** to *antibiotics"**
AUTHOR(S): Megraud F (REPRINT)
CORPORATE SOURCE: HOP PELLEGRIN,BACTERIOL ENFANTS LAB, PL AMELIE RABA LEON/F-33076 BORDEAUX//FRANCE/ (REPRINT); UNIV BORDEAUX,/BORDEAUX//FRANCE/
PUBLICATION TYPE: JOURNAL
PUBLICATION: ALIMENTARY PHARMACOLOGY & THERAPEUTICS, 1997, V11, ,1 (APR), P 43-53
GENUINE ARTICLE#: WX844

PUBLISHER: BLACKWELL SCIENCE LTD, OSNEY MEAD, OXFORD, OXON, ENGLAND OX2 0EL
ISSN: 0269-2813
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: *Resistance"** of *Helicobacter"** *pylori"** to *antibiotics"** included in current regimens used to eradicate H. *pylori"** is a major reason for failure. The definition of resistance is not simple, and the clinical relevance of in vitro results must be considered. The different methods of testing *antibiotics"** cannot apply in all cases, *Resistance"** to clarithromycin has a low prevalence rate (< 10%) and its mechanism is well defined (point *mutation"** on the *23S"** *rRNA"** genes, and decreased binding of the antibiotics to the ribosome). Its clinical relevance is not questioned and, because of a clear occurrence of a bimodal strain population, the method for *detecting"** resistance is not crucial. Resistance to nitroimidazoles is much more common, probably in the range of 30% or more in Europe, Neither the mechanism of action of metronidazole resistance nor its mechanism of is well known. The redox potential inside the cell which is important in reducing metronidazole to its active metabolite is probably a key element, but the exact metabolites involved are not yet known. Metronidazole resistance was found to be clinically relevant when standard triple therapy was used. The relevance is questioned for triple therapies including a proton pump inhibitor, clarithromycin and metronidazole, More clinical data are needed in this field and the use of agar dilutions is recommended to assess the susceptibility of H. *pylori"** to metronidazole.

The mechanism of resistance to quinolones has been described but these compounds are not currently used for H. *pylori"** infection. No resistance has yet been described for amoxycillin but continuous surveillance is needed in order to *detect"** new cases, as was recently the case for tetracycline resistance.

15/3,AB/26 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

13442193 BIOSIS NO.: 200200071014
*23S"** *rRNA"** *mutations"** and macrolide resistance in Campylobacter.
AUTHOR: Trieber C A(a); Taylor D E(a)
AUTHOR ADDRESS: (a)University of Alberta, Edmonton, AB**Canada
JOURNAL: IJMM International Journal of Medical Microbiology 291 (Supplement 31):p5 September, 2001
MEDIUM: print
CONFERENCE/MEETING: 11th International Workshop on Campylobacter, Helicobacter and related Organisms Freiburg, Germany September 01-05, 2001
ISSN: 1438-4221
RECORD TYPE: Citation
LANGUAGE: English
2001

15/3,AB/27 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

13410221 BIOSIS NO.: 200200039042

*Detection"** of point *mutations"** associated with *Helicobacter"** *pylori"** resistance to clarithromycin by real-time fluorescence based analysis.
AUTHOR: Momynaliev K T(a); Govorun V M(a); Isakov V A; Megraud F
AUTHOR ADDRESS: (a)Institute Physico-Chemical Medicine, Moscow**Russia
JOURNAL: Gut 49 (Supplement 11):pA10-A11 September, 2001
MEDIUM: print
CONFERENCE/MEETING: XIVth International Workshop on Gastroduodenal Pathology and Helicobacter pylori Strasbourg, France September 05-08, 2001
ISSN: 0017-5749
RECORD TYPE: Citation
LANGUAGE: English
2001

15/3,AB/28 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

13033406 BIOSIS NO.: 200100240555
Accurate prediction of macrolide resistance in *Helicobacter"** *pylori"** by a PCR line probe assay for *detection"** of *mutations"** in the *23S"** *rRNA"** Gene: Multicenter validation study.
AUTHOR: van Doorn Leen-Jan(a); Glupczynski Youri; Kusters Johannes G; Megraud Francis; Midolo Peter; Maggi-Solca Nadia; Queiroz Dulciene M M; Nouhan Nathalie; Stet Els; Quint Wim G V
AUTHOR ADDRESS: (a)Delft Diagnostic Laboratory, R. de Graafweg 7, 2625 AD, Delft: L.J.van.Doorn@ddl.nl**Netherlands
JOURNAL: Antimicrobial Agents and Chemotherapy 45 (5):p1500-1504 May, 2001
MEDIUM: print
ISSN: 0066-4804
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: *Helicobacter"** *pylori"** strains from 299 patients were tested in six laboratories in different countries. Macrolide susceptibility of the strains was *determined"** by agar dilution (17.4%) or the epsilometer test (82.6%). *Mutations"** in the 23S ribosomal DNA (rDNA) that are associated with macrolide resistance were analyzed by PCR and reverse hybridization (PCR-line probe assay (LiPA)). This method identifies A2115G, G2141A, A2142G, A2142C, A2142T, A2143G, and A2143C *mutations"** in the 23S rDNA. vacA s-region (s1a, s1b, s1c, and s2) and m-region (m1, m2a, and m2b) genotypes and cagA status were also *determined"** using another PCR-LiPA system. Of the 299 strains investigated by MIC testing, 130 (43.5%) were resistant and 169 (56.5%) were susceptible to clarithromycin. Of the 130 resistant strains, 127 (97.7%) contained 23S rDNA *mutations"**, whereas 167 (98.8%) of the 169 susceptible strains contained wild-type sequences. The predominant *mutations"** were A2143G (45.2%) and A2142G (33.3%). Twenty-eight (19.8%) strains contained multiple 23S rDNA *mutations"**. Only five resistant strains contained the A2142C *mutation"** (three of these in combination with the A2142G *mutation"**), and the A2115G, G2141A, A2142T, and A2143C *mutations"** were not found. MICs of clarithromycin for the A2142G *mutant"** strains were significantly higher than MICs for the A2143G strains. Although there was no significant association between

23S rDNA *mutations"** and the vacA and cagA status, clarithromycin-susceptible strains more often contained mixed vacA genotypes, indicating the presence of multiple H. *pylori"** strains. In conclusion, our data confirmed the very strong association between 23S rDNA *mutations"** and macrolide resistance and showed that the PCR-LiPA permits accurate and reliable diagnosis of macrolide resistance in H. *pylori"**.

2001

15/3,AB/29 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

10955802 BIOSIS NO.: 199799576947
*Detection"** of *23S"** *ribosomal"** *RNA"** gene *mutation"** associated with clarithromycin resistance using *Helicobacter"** *pylori"** specific primers.
AUTHOR: Maeda S; Ogura K; Kanai F; Yoshida H; Shiratori Y; Omata M
AUTHOR ADDRESS: Second Dep. Internal Med., Univ. Tokyo, Tokyo**Japan
JOURNAL: Gastroenterology 112 (4 SUPPL.):pA205 1997
CONFERENCE/MEETING: Digestive Disease Week and the 97th Annual Meeting of the American Gastroenterological Association Washington, D.C., USA May 11-14, 1997
ISSN: 0016-5085
RECORD TYPE: Citation
LANGUAGE: English
1997

15/3,AB/30 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

10834013 BIOSIS NO.: 199799455158
A PCR-oligonucleotide ligation assay to *determine"** the prevalence of *23S"** *rRNA"** gene *mutations"** in clarithromycin-resistant *Helicobacter"** *pylori"**.
AUTHOR: Stone Gregory G(a); Shortridge Dee; Versalovic James; Beyer Jull; Flamm Robert K; Graham David Y; Ghoneim Adeeb T; Tanaka S Ken
AUTHOR ADDRESS: (a)Abbott Lab., Dep. 47T, Build. AP3, 100 Abbott Park Rd., Abbott Park, IL 60064**USA
JOURNAL: Antimicrobial Agents and Chemotherapy 41 (3):p712-714 1997
ISSN: 0066-4804
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We have developed a rapid PCR-oligonucleotide ligation assay that can discriminate single base substitutions that are associated with clarithromycin resistance in *Helicobacter"** *pylori"**. Susceptible isolates were wild type at positions 2143 and 2144 (cognate to 2058 and 2059 in Escherichia coli), while 93% of the resistant isolates contained A-to-G *mutations"** at either position and 7% of the isolates contained A-to-C *mutations"** at position 2143. In addition, the MIC for 86% of the resistant isolates with an A2143 *mutation"** was gtoreq 64 mu-g per ml, and that for 89% of the resistant isolates with an A2144 *mutation"** was ltoreq 32 mu-g per ml.

1997

15/3,AB/31 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

11086336 21086962 PMID: 11218414
Mechanism of drug resistance in *Helicobacter"** *pylori"**]
Maeda S; Yoshida H
Department of Gastroenterology, Faculty of Medicine, University of Tokyo.
Nippon rinsho. Japanese journal of clinical medicine (Japan) Feb 2001, 59 (2) p367-73, ISSN 0047-1852 Journal Code: 0420546
Document type: Journal Article; Review; Review, Tutorial ; English Abstract
Languages: JAPANESE
Main Citation Owner: NLM
Record type: Completed
Clarithromycin is one of the most important antibiotics for H. *pylori"** eradication. However, 5-10% was reported to be resistant. It has been shown that one point *mutation"** in the *23S"** *rRNA"** gene is associated with resistance to clarithromycin. To *detect"** H. *pylori"** infection and the *mutation"** simultaneously, we have designed PCR primers specific for H. *pylori"** , and established assays of PCR-RFLP and PCR-preferential homo-duplex formation (PHFA). Using this assay, we can *detect"** mixed infections with wild and *mutant"**-strains. The prevalence of *mutant"** infection increased through clarithromycin-based eradication. However, the existence of *mutant"** strains had been confirmed before therapy in most cases who 'converted' to *mutant"** after therapy. Metronidazole is also one of the most important antibiotics for eradication. However, 5-50% was reported to be resistant. It has been shown that rdx gene *mutation"** is associated with resistance. It is reported that inactivation of the rdx gene is frequently, but not always, associated with resistance to metronidazole. Amoxicillin resistant strains were rare (1.2% in Japanese strains). It is reported that penicillin-binding protein might play a role in the resistance. By *detecting"** of the resistance based on the molecular mechanism, patients can be treated with adequate *antibiotics"** with information about *resistance"**.

15/3,AB/32 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10172538 99155992 PMID: 10036941
*Detection"** of *Helicobacter"** *pylori"** *23S"** *rRNA"** gene *mutation"** associated with clarithromycin resistance and its clinical applicability]
Maeda S; Yoshida H
Department of Gastroenterology, University of Tokyo.
Nippon rinsho. Japanese journal of clinical medicine (JAPAN) Jan 1999, 57 (1) p87-92, ISSN 0047-1852 Journal Code: 0420546
Document type: Journal Article; Review; Review, Tutorial ; English Abstract
Languages: JAPANESE
Main Citation Owner: NLM
Record type: Completed
Clarithromycin is one of the most important antibiotics for H. *pylori"** eradication. However, 5-10% was reported to be resistant. It has been shown

that one point *mutation"** in the *23S"** *rRNA"** gene is associated with resistance to clarithromycin. We confirmed that this finding applied to the isolates in Japan. To *detect"** H. *pylori"** infection and the *mutation"** simultaneously, we have designed PCR primers specific for H. *pylori"** , and established assays of PCR-RFLP and PCR-preferential homo-duplex formation (PHFA). Compared with other conventional methods, these assays achieved above 95% sensitivity. It is also demonstrated that the eradication rates achieved by clarithromycin-based regimens significantly differed between *mutant"** and wild type infections. By *detecting"** of *23S"** *rRNA"** gene *mutations"** associated with clarithromycin resistance, patients can be treated with adequate *antibiotics"** with information about *resistance"**.

15/3,AB/33 (Item 1 from file: 73)
DIALOG(R)File 73:EMBASE

11627585 EMBASE No: 2002199695
Direct *detection"** of *Helicobacter"** *pylori"** *mutations"** associated with macrolide resistance in gastric biopsy material taken from human immunodeficiency virus-infected subjects
Scarpellini P.; Carrera P.; Cavallero A.; Cernuschi M.; Mezzi G.; Testoni P.A.; Zingale A.; Lazzarin A.
P. Scarpellini, Infectious Diseases Division, San Raffaele Scientific Institute, Via Stamira D'Ancona 20, 20127 Milan Italy
AUTHOR EMAIL: scarpellini.paolo@hsr.it
Journal of Clinical Microbiology (J. CLIN. MICROBIOL.) (United States) 2002, 40/6 (2234-2237)
CODEN: JCMID ISSN: 0095-1137
DOCUMENT TYPE: Journal ; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 24

One hundred forty gastric biopsies were tested by microbiological methods and by amplifying a sequence of *23S"** *rRNA"** and identifying *mutations"** associated to clarithromycin resistance. Seventy-six specimens were positive for *Helicobacter"** *pylori"**. *Mutational"** analysis revealed alterations in 18 (39.1%) of 46 and 2 (8.7%) of 23 samples from human immunodeficiency virus-seropositive and -seronegative persons, respectively. The results of the *mutational"** analysis fully correlated with those of the susceptibility tests.

15/3,AB/34 (Item 2 from file: 73)
DIALOG(R)File 73:EMBASE

11562460 EMBASE No: 2002136982
Validation of diffusion methods for macrolide susceptibility testing of *Helicobacter"** *pylori"**
Grignon B.; Tankovic J.; Megraud F.; Glupczynski Y.; Husson M.O.; Conroy M.C.; Emond J.P.; Loulergue J.; Raymond J.; Fauchere J.L.
Prof. J.L. Fauchere, Microbiologie A, CHU La Miletrie, BP 577, 86021 Poitiers France
AUTHOR EMAIL: j.l.fauchere@chu-poiliers.fr
Microbial Drug Resistance (MICROB. DRUG RESIST.) (United States) 2002, 8/1 (61-66)

CODEN: MDREF ISSN: 1076-6294
DOCUMENT TYPE: Journal ; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 25

*Helicobacter"** *pylori"** resistance to macrolides is increasing, and the need for susceptibility testing has become crucial. The only standardized method is agar dilution, which is not adapted to clinical practice. The present work aimed: (1) to optimize the technical conditions and to assess the reproducibility of the E-test and disk diffusion method for macrolides susceptibility testing of H. *pylori"**, and (2) to assess the performances of these two phenotypic methods in *detecting"** strains harboring a resistance mechanism to macrolides. We used 191 isolates collected in nine centers of France and Belgium. Phenotypic tests were performed on Mueller-Hinton agar supplemented with 10 % horse blood, inoculated with a 2-day-old H. *pylori"** suspension (10SUP8 CFU/ml), and incubated for 72 hr at 37degreesC under microaerophilic conditions. The reproducibility studied on two randomly selected strains was better for disk diffusion than for the E-test for both clarithromycin and erythromycin. For a subset of 10 strains, the MICs of erythromycin and clarithromycin did not differ from more than one two-fold dilution when *determined"** by E-test or agar dilution method. The breakpoints were for MICs: 1 mg/L for both clarithromycin and erythromycin and for inhibition diameters, 22 mm for clarithromycin and 17 mm for erythromycin. There was a 100% concordance between susceptibility to erythromycin and clarithromycin. However, the susceptible and resistant populations were better separated by testing erythromycin. Of 34 resistant strains, two lacked the A2142G and A2143G point *mutations"** in *23S"** *rRNA"** by PCR-RFLP. None of 15 tested sensitive strains were positive for one of these two point *mutations"**. For clinical practice, we recommend to assess macrolide susceptibility of H. *pylori"** by using one of these two phenotypic methods under the described technical conditions.

15/3,AB/35 (Item 3 from file: 73)
DIALOG(R)File 73:EMBASE

11548209 EMBASE No: 2002119176
PCR-restriction fragment length *polymorphism"** can also *detect"** point *mutation"** A2142C in the *23S"** *rRNA"** gene, associated with *Helicobacter"** *pylori"** resistance to clarithromycin [1]
Menard A.; Santos A.; Megraud F.; Oleastro M.
A. Menard, Laboratoire de Bacteriologie, Universite Victor Segalen Bordeaux 2, Bordeaux France
AUTHOR EMAIL: Armelle.Menard@labhel.u-bordeaux2.fr
Antimicrobial Agents and Chemotherapy (ANTIMICROB. AGENTS CHEMOTHER.) (United States) 2002, 46/4 (1156-1157)
CODEN: AMACC ISSN: 0066-4804
DOCUMENT TYPE: Journal ; Letter
LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 15

15/3,AB/36 (Item 4 from file: 73)
DIALOG(R)File 73:EMBASE

11439773 EMBASE No: 2002011425
Assessment of clarithromycin-resistant *Helicobacter"** *pylori"** among patients in Shanghai and Guangzhou, China, by primer-mismatch PCR
Pan Z.-J.; Su W.-W.; Tytgat G.N.J.; Dankert J.; Van der Ende A.
A. Van der Ende, Department of Medical Microbiology, Academic Medical Center, University of Amsterdam, P.O. Box 22700, 1100 DE Amsterdam Netherlands
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Journal of Clinical Microbiology (J. CLIN. MICROBIOL.) (United States) 2002, 40/1 (259-261)
CODEN: JCMID ISSN: 0095-1137
DOCUMENT TYPE: Journal ; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 19

Of 96 *Helicobacter"** *pylori"** isolates from patients in Shanghai and Guangzhou, China, 5 had the A2143G *23S"** *rRNA"** *mutation"** as *determined"** by primer-mismatch PCR and were resistant to clarithromycin by the E-test. The remaining isolates were primer-mismatch PCR negative and susceptible to clarithromycin. The conclusion is that the prevalence of clarithromycin-resistant H. *pylori"** isolates among these Chinese patients is 5%.

15/3,AB/37 (Item 5 from file: 73)
DIALOG(R)File 73:EMBASE

11425345 EMBASE No: 2001440370
Update on *Helicobacter"** *pylori"** *resistance"** to *antibiotics"**
Megraud F.
F. Megraud, Centre National de Reference, Campylobacters et Helicobacters, Hopital Pellegrin, Place Amelie Raba-Leon, 33076 Bordeaux Cedex France
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Antibiotiques (ANTIBIOTIQUES) (France) 2001, 4/3 (215-224)
CODEN: ANTBF ISSN: 1294-5501
DOCUMENT TYPE: Journal ; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 80

*Helicobacter"** *pylori"** is essentially concerned by resistance occurring by point *mutations"**. Macrolide resistance is the most clinically relevant problem because it leads to an important decrease in the efficacy of the triple therapies used (2 antibiotics + proton pump inhibitor). However, because only 2 nucleotides of the *23S"** *rRNA"** are involved, this resistance is easy to *detect"** using genotypic methods. In contrast, metronidazole resistance concerns several genes (rdxA, frxA) and several nucleotides can be implicated which makes it impossible to apply a genotypic approach for its *detection"**. Fortunately, this resistance has less impact on the clinical outcome (20%) using current triple therapies. Resistance to amoxicillin is rare and still controversial; tolerant strains have been isolated. Point *mutations"** are also responsible for resistance to quinolones (gyrA) and rifamycins (rpoB), antibiotics less commonly used to treat this infection. In 2000, the resistance rate of H. *pylori"** in France was estimated to be 18% for clarithromycin and 25-30 % for metronidazole.

15/3,AB/38 (Item 6 from file: 73)
DIALOG(R)File 73:EMBASE

11182964 EMBASE No: 2001197378
Relationship between clarithromycin breakpoint for *Helicobacter"** *pylori"** and point *mutation"** in *23S"** *rRNA"** gene
Kobayashi I.; Saika T.; Muraoka H.; Inoue M.; Nasu M.
I. Kobayashi, Chemotherapy Division, Mitusbishi Kagaku Bio-Clinical Lab., 3-30-1 Shimura, Itabashi-ku, Tokyo 174-8555 Japan
Japanese Journal of Chemotherapy (JPN. J. CHEMOTHER.) (Japan) 2001, 49/4 (236-240)
CODEN: NKRZE ISSN: 1340-7007
DOCUMENT TYPE: Journal ; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

The resistance of *Helicobacter"** *pylori"** to clarithromycin (CAM) is mainly due to adenine (A)-to-guanine (G) point *mutations"** at the A 2142 or A 2143 of the *23S"** *rRNA"** gene. In this study, CAM MICs for 302 clinical isolates of H. *pylori"** were *determined"** by agar dilution based on the guideline (M 100-S 10) established by the National Committee for Clinical Laboratory Standards (NCCLS). The relationship between the CAM breakpoint for H. *pylori"** and the point *mutation"** in the *23S"** *rRNA"** gene was studied. When H. *pylori"** strains isolated in advance from patients in whom strains were eradicated with CAM therapy were tested, CAM MICs for 258 (98.5%) of the 262 isolates ranged from <=0.015 to 0.5 mug/mL. CAM MICs for 23 (57.5%) and 17 (42.5%) of 40 strains isolated from patients in whom strains were not eradicated with CAM therapy were <=0.25 mug/mL and >=4 mug/mL. The 4 H. *pylori"** strains (MIC; >=8mug/mL) isolated from patients in whom strains were eradicated had A 2143 G *mutation"**, and 17 strains (>=4mug/mL) from patients in whom strains were not eradicated had A 2143 G and A 2142 G *mutations"**. H. *pylori"** isolates belonging to the S (MIC; <=0.25 mug/mL) or I (0.5 mug/mL) category in the NCCLS guideline did not possess any type of *mutation"** in the *23S"** *rRNA"** gene, but all isolates belonging to the R category (>= 1 mug/mL) had point *mutations"**. It is thus noteworthy that CAM breakpoint MICs for H. *pylori"** based on the NCCLS guideline agreed with point *mutations"** in the *23S"** *rRNA"** gene of test isolates.

15/3,AB/39 (Item 7 from file: 73)
DIALOG(R)File 73:EMBASE

11120591 EMBASE No: 2001133053
PCR-based diagnosis of *Helicobacter"** *pylori"** infection and real-time *determination"** of clarithromycin resistance directly from human gastric biopsy samples
Chisholm S.A.; Owen R.J.; Louise Teare E.; Saverymuttu S.
R.J. Owen, Helicobacter Reference Unit, Laboratory of Enteric Pathogens, Central Public Health Laboratory, 61 Colindale Ave., Colindale, London NW9 5HT United Kingdom
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Journal of Clinical Microbiology (J. CLIN. MICROBIOL.) (United States) 2001, 39/4 (1217-1220)
CODEN: JCMID ISSN: 0095-1137
DOCUMENT TYPE: Journal ; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 25

A novel PCR *detection"** assay that amplifies the *Helicobacter"** *pylori"**-specific vacuolating cytotoxin gene (vacA) and thus enables rapid diagnosis of infection is described. Additionally, a real-time probe hybridization melting point analysis assay to *detect"** all three *mutations"** in the *23S"** *rRNA"** gene associated with clarithromycin resistance was applied directly to antral gastric biopsy samples. Comparison with culture and an alternative PCR assay targeting the 16S rrn gene showed that the vacA assay was sensitive and specific when tested on biopsy samples from 121 patients. Clarithromycin susceptibilities could be *determined"** in the majority (92.3%) of culture-positive gastric biopsy samples analyzed, four of which generated melting peaks indicative of clarithromycin resistance by either an A-->G or A-->C *mutation"**. The presence of the *mutations"** correlated with the clarithromycin disk diffusion sensitivities of matched cultures. This PCR-based system was simple to perform and could be completed in 3 to 4 h, thereby overcoming the delays associated with conventional culture methods for H. *pylori"** identification and susceptibility testing.

15/3,AB/40 (Item 8 from file: 73)
DIALOG(R)File 73:EMBASE

11018076 EMBASE No: 2001066004
Rapid *detection"** of *mutations"** in the *23S"** *rRNA"** gene of *Helicobacter"** *pylori"** that confers resistance to clarithromycin treatment to the bacterium
Matsumura M.; Hikiba Y.; Ogura K.; Togo G.; Tsukuda I.; Ushikawa K.; Shiratori Y.; Omata M.
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Journal of Clinical Microbiology (J. CLIN. MICROBIOL.) (United States) 2001, 39/2 (691-695)
CODEN: JCMID ISSN: 0095-1137
DOCUMENT TYPE: Journal ; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 14

We developed a new method capable of *detecting"** point *mutations"** in the *23S"** *rRNA"** gene of *Helicobacter"** *pylori"** using a LightCycler. Our method can *detect"** a *mutation"** in this gene in less than I h and can process many samples at once, thereby contributing to the selection of patients suitable for clarithromycin-based therapy.

15/3,AB/41 (Item 9 from file: 73)
DIALOG(R)File 73:EMBASE

10887800 EMBASE No: 2000376446
Clarithromycin resistance stability in *Helicobacter"** *pylori"**: Influence of the MIC and type of *mutation"** in the *23S"** *rRNA"**
Alarcon T.; Domingo D.; Prieto N.; Lopez-Brea M.
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Journal of Antimicrobial Chemotherapy (J. ANTIMICROB. CHEMOTHER.) (United Kingdom) 2000, 46/4 (613-616)
CODEN: JACHD ISSN: 0305-7453
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 10

Thirty clarithromycin-resistant *Helicobacter"** *pylori"** strains (MIC range 8-64 mg/L) were subcultured in a drug-free medium and the MIC was *determined"** every five passages to *detect"** in vitro stability of resistance. Three out of the 30 (10%) lost their resistance after 10, 13 or 18 subcultures (MIC decrease from 8 to 0.008, from 16 to 0.064 and from 32 to 0.016 mg/L). The effect of four macrolides at subinhibitory concentrations on the development of resistance was studied in H. *pylori"** NCTC 11638 and TIGR 26695. A change in the MIC was observed only when NCTC11638 was exposed to 0.5 x MIC of erythromycin for 20 days.

15/3,AB/42 (Item 10 from file: 73)
DIALOG(R)File 73:EMBASE

10869790 EMBASE No: 2000351315
Clarithromycin-resistance and point *mutations"** in the *23S"** *rRNA"** gene in *Helicobacter"** *pylori"** isolates from Japan
Umegaki N.; Shimoyama T.; Nishiya D.; Suto T.; Fukuda S.; Munakata A.
Dr. T. Shimoyama, First Dept. of Internal Medicine, Hirosaki Univ. School of Medicine, 5 Zaifu-cho, Hirosaki 036-8562 Japan
AUTHOR EMAIL: tsimo-hki@umin.u-tokyo.ac.jp
Journal of Gastroenterology and Hepatology (J. GASTROENTEROL. HEPATOL.) (Australia) 2000, 15/8 (906-909)
CODEN: JGHEE ISSN: 0815-9319
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 17

Background: Resistance of *Helicobacter"** *pylori"** to clarithromycin is mostly due to the point *mutations"** in the *23S"** *rRNA"**. In Japan, however, the frequency of these *mutations"** has not been fully investigated. Furthermore, no study has used gastric biopsy specimens to *detect"** these point *mutations"**. Methods: The frequency of primary clarithromycin-resistant H. *pylori"** was examined by polymerase chain reaction-restriction fragment length *polymorphism"** (PCR-RFLP). Eighty-two strains (42 isolated from patients with gastric cancer and 40 isolated from patients with chronic gastritis) were examined. Two biopsy specimens obtained from patients in whom eradication therapy including clarithromycin had failed were also studied. Results: Either A2143G or A2144G point *mutation"** was *detected"** in 90% of clarithromycin-resistant H. *pylori"** strains. Eight out of 82 strains (9.8%) had either A2143G or A2144G point *mutation"**. Only one out of 42 strains in patients with gastric cancer had A2143G *mutation"**, whereas five strains had A2144G and two had A2143G *mutations"** in 40 strains isolated from control subjects. The proportion was significantly lower in patients with early gastric cancer (P< 0.05). This PCR-RFLP was also applicable for DNA samples extracted from biopsy specimens and infection of clarithromycin-resistant H. *pylori"** was observed. Conclusion: The

results suggest that the point *mutation"** in the *23S"** *rRNA"** gene is commonly seen in clarithromycin-resistant H. *pylori"** and it contributes to the treatment failure in Japan. The PCR-RFLP system is a sensitive method by which to diagnose H. *pylori"** infection as well as a simple method for *detecting"** clarithromycin resistance without bacterial culture. (C) 2000 Blackwell Science Asia Pry Ltd.

15/3,AB/43 (Item 11 from file: 73)
DIALOG(R)File 73:EMBASE

10591455 EMBASE No: 2000056694
PCR using 3'-mismatched primers to *detect"** A2142C *mutation"** in *23S"** *rRNA"** conferring resistance to clarithromycin in *Helicobacter"** *pylori"** clinical isolates
Alarcon T.; Domingo D.; Prieto N.; Lopez-Brea M.
T. Alarcon, Department of Microbiology, Hosp. Universitario de la Princesa, Diego de Leon 62, Madrid 28006 Spain
AUTHOR EMAIL: microbiologia@hup.es
Journal of Clinical Microbiology (J. CLIN. MICROBIOL.) (United States) 2000, 38/2 (923-925)
CODEN: JCMID ISSN: 0095-1137
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 21

Twenty-five clarithromycin-resistant *Helicobacter"** *pylori"** strains (selected by agar dilution) were studied to *detect"** A2142G and A2143G *mutations"** in the *23S"** *rRNA"** gene by a PCR-restriction fragment length *polymorphism"** method and an A2142C *mutation"** by using a 3'-mismatched specific primer. A 700-bp amplified fragment was obtained by the mismatched PCR only in strains without an A2142G or A2143G *mutation"** , indicating that those strains had the A2142C *mutation"**.

15/3,AB/44 (Item 12 from file: 73)
DIALOG(R)File 73:EMBASE

10566500 EMBASE No: 2000029798
*Detection"** of clarithromycin-resistant *Helicobacter"** *pylori"** strains by a preferential homoduplex formation assay
Maeda S.; Yoshida H.; Matsunaga H.; Ogura K.; Kawamata O.; Shiratori Y.; Omata M.
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Journal of Clinical Microbiology (J. CLIN. MICROBIOL.) (United States) 2000, 38/1 (210-214)
CODEN: JCMID ISSN: 0095-1137
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 31

It has been shown that resistance to clarithromycin, a major cause of failure in *Helicobacter"** *pylori"** eradication therapy, is associated with point *mutations"** in the *23S"** *rRNA"** gene. We sought to apply

the preferential homoduplex formation assay (PHFA), a novel technique for the efficient *detection"** of point *mutations"**, to *detection"** of the *mutations"**. PHFA was performed on streptavidin-coated microtiter plates with biotin- and dinitrophenyl-labeled amplicons to *detect"** the wild-type gene or each *mutant"** gene. DNA samples were extracted from gastric juice specimens of 412 patients with H. *pylori"** infection and were applied to the assay. The *detection"** threshold of PHFA was as few as 10 gene copies. The sensitivity of PHFA for the *detection"** of H. *pylori"** infection was higher than those of culture and the rapid urease test. A total of 337 (81.8%) samples had the wild-type gene, 38 (9.2%) had the A2144G *mutation"**, and 37 (9.0%) contained both the wild type and a *mutation"** (A2144G in 30 samples, A2143G in 5 samples, and A2143G plus A2144G in 2 samples). About half the strains isolated from patients with mixed infection were susceptible by the agar dilution method (MIC, <0.1 mg/liter). Therefore, PHFA can *detect"** clarithromycin-resistant H. *pylori"** strains, even in patients with mixed infections with the wild type, that are not *detectable"** by the agar dilution method.

15/3,AB/45 (Item 13 from file: 73)
DIALOG(R)File 73:EMBASE

07765742 EMBASE No: 1999248872
Rapid *detection"**, by PCR and reverse hybridization, of *mutations"** in the *Helicobacter"** *pylori"** *23S"** *rRNA"** gene, associated with macrolide resistance
Van Doorn L.-J.; Debets-Ossenkopp Y.J.; Marais A.; Sanna R.; Megraud F.; Kusters J.G.; Quint W.G.V.
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Antimicrobial Agents and Chemotherapy (ANTIMICROB. AGENTS CHEMOTHER.) (United States) 1999, 43/7 (1779-1782)
CODEN: AMACC ISSN: 0066-4804
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 21

A PCR-based reverse hybridization system (research prototype kit INNO-LiPA for H. *pylori"** resistance) was developed and evaluated for simultaneous *detection"** of 23S ribosomal DNA point *mutations"**, associated with macrolide resistance in *Helicobacter"** priori. Fifty-seven H. *pylori"** strains (51 natural, 6 laboratory-derived artificial, 52 resistant, and 5 susceptible strains) were tested by PCR-LiPA (*detecting"** *mutations"** A2115<rt arrow>G, G2141<rt arrow>A, A2142<rt arrow>G, A2142<rt arrow>C, A2143<rt arrow>G, A2143<rt arrow>C, and A2143<rt arrow>T), DNA sequencing, restriction fragment length *polymorphism"**, and/or hybridization to oligonucleotide probes. Results were highly concordant, but PCR-LiPA appears to be more sensitive for the simultaneous *detection"** of multiple *mutants"**.

15/3,AB/46 (Item 14 from file: 73)
DIALOG(R)File 73:EMBASE

07649798 EMBASE No: 1999130440

Direct *detection"** of *Helicobacter"** *pylori"** resistance to macrolides by a polymerase chain reaction/DNA enzyme immunoassay in gastric biopsy specimens

Marais A.; Monteiro L.; Occhialini A.; Pina M.; Lamouliatte H.; Megraud F.

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Gut (GUT) (United Kingdom) 1999, 44/4 (463-467)
CODEN: GUTTA ISSN: 0017-5749
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 21

Background - The increasing use of macrolides especially in the treatment of *Helicobacter"** *pylori"** infection has led to an increase in resistant strains. The resistance of H *pylori"** to macrolides, especially clarithromycin, is one of the major causes of eradication failure. In H *pylori"**, clarithromycin resistance is due to point *mutations"** localised in domain V of *23S"** *rRNA"**. Aim - To develop a molecular technique based on amplification of a relevant fragment of the *23S"** *rRNA"** and colorimetric hybridisation in liquid phase to *detect"** directly in biopsy specimens the type of *mutation"** associated with resistance of H *pylori"** to clarithromycin. Methods - Gastric biopsy samples from 61 patients were submitted to this test. The results were compared with standard methods (*determination"** of minimal inhibition concentration, polymerase chain reaction/restriction fragment length *polymorphism"**, and/or DNA sequencing) in order to evaluate the test and to define the cut off values, specificity, and sensitivity. Results - The 14 biopsy samples in which H *pylori"** was not *detected"** did not give positive result in any assay, and the 14 samples harbouring strains susceptible to clarithromycin gave a positive result with the wild type probe as expected. The 33 biopsy specimens containing resistant strains always gave a positive signal with one of the probes *detecting"** resistant organisms, but in eight cases they also reacted with the wild type probe, indicating that a mixture of resistant and susceptible organisms was present. Conclusion - The importance of this new assay is that it allows the *detection"** of multiple genotypes corresponding to either heterogeneous genotypes or mixed infections. Moreover, it allows in a single step not only the *detection"** of H *pylori"** but also the *determination"** of its susceptibility to clarithromycin directly in biopsy specimens without the need for culture.

15/3,AB/47 (Item 15 from file: 73)
DIALOG(R)File 73:EMBASE

07439402 EMBASE No: 1998351368
*Detection"** of point *mutations"** associated with resistance of *Helicobacter"** *pylori"** to clarithromycin by hybridization in liquid phase

Pina M.; Occhialini A.; Monteiro L.; Doermann H.-P.; Megraud F.

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Journal of Clinical Microbiology (J. CLIN. MICROBIOL.) (United States) 1998, 36/11 (3285-3290)
CODEN: JCMID ISSN: 0095-1137

DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 25

When the standard procedure for *determining"** antibiotic susceptibility of bacteria is used, the results are delayed, especially for bacteria that grow slowly, such as *Helicobacter"** *pylori"**. Treatment for this bacterium may involve clarithromycin, a compound for which resistance has been associated with point *mutations"** on the *23S"** *rRNA"** gene. This resistance is currently found in organisms isolated from 0 to 15% of patients and jeopardizes the success of the treatment. We have designed a test involving amplification and colorimetric hybridization in the liquid phase to *detect"** the *mutation"** at the molecular level. First, four reference strains, including the wild type and three strains with the *mutations"** A2143C, A2143G, and A2144G, were used to optimize the method. Amplification was carried out with primers previously published. The amplified products were added to probe-coated microtiter wells. A DNA enzyme immunoassay was used to *detect"** the hybrids. The optimal conditions of the hybridization were defined for each probe. Nineteen H. *pylori"** strains resistant to clarithromycin and 22 susceptible according to phenotypic data were submitted to restriction with BsaI and BbsI, and part of the *23S"** *rRNA"** gene was sequenced in order to *determine"** the *mutation"** involved for the resistant strains. The new assay showed a complete correlation with the reference methods, except for one strain. Crosshybridizations as well as application of the reaction to other bacteria did not lead to optical densities higher than the cutoff values chosen with the receiving operating characteristic curve. This method can be easily standardized and gives a result within a day. Its application directly to the biopsy specimens or infected gastric juice is planned in the future.

15/3,AB/48 (Item 16 from file: 73)
DIALOG(R)File 73:EMBASE

07397428 EMBASE No: 1998305311
*Helicobacter"** *pylori"** specific nested PCR assay for the *detection"** of *23S"** *rRNA"** *mutation"** associated with clarithromycin resistance

Maeda S.; Yoshida H.; Ogura K.; Kanai F.; Shiratori Y.; Omata M.
Dr. S. Maeda, Second Dept. of Internal Medicine, Faculty of Medicine, University of Tokyo, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113 Japan
Gut (GUT) (United Kingdom) 1998, 43/3 (317-321)
CODEN: GUTTA ISSN: 0017-5749
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 21

Background-Clarithromycin is one of the most important antibiotics for *Helicobacter"** *pylori"** eradication. However, 5-10% of strains are reported to be resistant. It has been shown that one point *mutation"** in the *23S"** *rRNA"** gene is associated with resistance to clarithromycin. Aims-To establish a polymerase chain reaction (PCR) system which amplifies a segment of the *23S"** *rRNA"** gene containing the *mutation"** points with primers specific for H *pylori"**, so that H *pylori"** infection and the *mutation"** associated with clarithromycin resistance can be examined simultaneously. Methods-To *detect"** H *pylori"** infection and the

*mutation"** simultaneously, primers specific for the H *pylori"** *23S"** *rRNA"** gene were designed based on sequence conservation among H *pylori"** strains and sequence specificity as compared with other bacteria. DNA from 57 cultured strains and from 39 gastric juice samples was amplified in the seminested *23S"** *rRNA"** PCR. Clinical applicability was evaluated in 85 patients. Results-DNA samples from 57 cultured strains were all amplified. The novel assay and the urease A PCR agreed in 37/39 gastric juice samples with no false positives. The assay did not amplify the DNA of bacteria other than H *pylori"**. Eight of 85 samples had the *mutation"** before treatment. In clarithromycin based treatment, eradication was achieved in 2/5 (40%) with the *mutation"** and 29/34 (85%) without the *mutation"**. Conclusion-The assay using gastric juice is quick (within 12 hours) and noninvasive (endoscopy not required), enabling rapid initiation of appropriate antibiotic treatment.

15/3,AB/49 (Item 17 from file: 73)
DIALOG(R)File 73:EMBASE

06812077 EMBASE No: 1997094567
Evaluation of rapid molecular methods for *detection"** of clarithromycin resistance in *Helicobacter"** *pylori"**
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F. Szczebara, Laboratoire Bacteriologie-Hygiene, Faculte de medecine, 1 place de Verdun, 59045 Lille cedex France
European Journal of Clinical Microbiology and Infectious Diseases (EUR. J. CLIN. MICROBIOL. INFECT. DIS.) (Germany) 1997, 16/2 (162-164)
CODEN: EJCDE ISSN: 0934-9723
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 14

Resistance of *Helicobacter"** *pylori"** to clarithromycin is due to point *mutations"** at position A2143 or A2144 of the rrnH *23S"** *rRNA"** gene, each *mutation"** creating an additional restriction site for BsaI or MboII. A procedure combining PGR and RFLP analysis was evaluated for *detection"** of these *mutations"** using primers specific for the *23S"** *rRNA"** gene, and BsaI and MboII enzymes. All clarithromycin-resistant isolates (8/8), as defined by the MIC, were found to be resistant by PCR-RFLP. No clarithromycin-sensitive isolates (14/14) gave a positive reaction.

15/3,AB/50 (Item 1 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

132246830 CA: 132(19)246830e JOURNAL
Novel method for rapid determination of clarithromycin sensitivity in Helicobacter pylori
AUTHOR(S): Gibson, J. R.; Saunders, N. A.; Burke, B.; Owen, R. J.
LOCATION: Helicobacter Reference Unit, Laboratory of Enteric Pathogens, Central Public Health Laboratory, London, UK, NW9 5HT
JOURNAL: J. Clin. Microbiol. DATE: 1999 VOLUME: 37 NUMBER: 11 PAGES: 3746-3748 CODEN: JCMIDW ISSN: 0095-1137 LANGUAGE: English PUBLISHER: American Society for Microbiology

15/3,AB/51 (Item 2 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

132020800 CA: 132(3)20800h PATENT
Determination of antibiotic resistance of microorganisms by in situ hybridization using mutation-specific 23S rRNA-targetted oligonucleotide probes
INVENTOR(AUTHOR): Haas, Rainer; Trebesius, Karlheinz; Apfel, Heiko
LOCATION: Germany,
ASSIGNEE: Creatogen Biosciences G.m.b.H.
PATENT: PCT International ; WO 9961660 A1 DATE: 19991202
APPLICATION: WO 99EP3527 (19990521) *DE 19823098 (19980522) *DE 19916610 (19990413)
PAGES: 84 pp. CODEN: PIXXD2 LANGUAGE: German CLASS: C12Q-001/68A
DESIGNATED COUNTRIES: AE; AL; AM; AT; AU; AZ; BA; BB; BG; BR; BY; CA; CH; CN; CU; CZ; DE; DK; EE; ES; FI; GB; GD; GE; GH; GM; HR; HU; ID; IL; IN; IS; JP; KE; KG; KP; KR; KZ; LC; LK; LR; LS; LT; LU; LV; MD; MG; MK; MN; MW; MX; NO; NZ; PL; PT; RO; RU; SD; SE; SG; SI; SK; SL; TJ; TM; TR; TT; UA; UG; US; UZ; VN; YU; ZA; ZW; AM; AZ; BY; KG; KZ; MD; RU; TJ; TM
DESIGNATED REGIONAL: GH; GM; KE; LS; MW; SD; SL; SZ; UG; ZW; AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE; BF; BJ; CF; CG; CI; CM; GA; GN; GW; ML; MR; NE; SN; TD; TG

15/3,AB/52 (Item 1 from file: 144)
DIALOG(R)File 144:Pascal

14996846 PASCAL No.: 01-0152078
Spontaneous *mutations"** that confer *antibiotic"** *resistance"** in *Helicobacter"** *pylori"**
GE WANG; WILSON Trevor J M; QIN JIANG; TAYLOR Diane E
Department of Medical Microbiology and Immunology, University of Alberta, Edmonton, Alberta, Canada
Journal: Antimicrobial agents and chemotherapy, 2001, 45 (3) 727-733
Language: English
In this study, we systematically examined in vitro frequencies and spectra of the spontaneous *mutations"** in *Helicobacter"** *pylori"** that confer resistance to clarithromycin (Cla SUP r), metronidazole (Mtz SUP r), amoxicillin (Amx SUP r), ciprofloxacin (Cip SUP r), and rifampin (Rif SUP r). The *mutation"** rate of Rif SUP r or Cip SUP r *determined"** in a fluctuation assay is 1 x 10 SUP - SUP 8 to 2 x 10 SUP - SUP 8 per cell per division. In contrast, the *mutation"** rates of Cla SUP r , Mtz SUP r , and Amx SUP r are much lower (<10 SUP - SUP 9). However, Mtz SUP r *mutants"** could be readily selected in vitro by using the serial passage method, suggesting that the *mutagenic"** effect and selective effect of a sublethal dose of metronidazole contribute to the rapid development of Mtz SUP r . Analysis of spontaneous Rif SUP r , Cla SUP r , and Cip SUP r *mutants"** confirmed previous results indicating that *mutations"** within the rpoB gene, the *23S"** *rRNA"** gene, and the gyrA gene, respectively, are responsible; also, several new *mutant"** alleles were identified. Mtz SUP r *mutants"** resulted most frequently, but not always, from *mutations"** in the rdxA gene. DNA fragments containing each *mutant"** allele could readily transform susceptible H. *pylori"** strains to resistance, confirming that each *mutant"** allele is responsible for the resistance phenotype.

15/3,AB/53 (Item 1 from file: 348)
DIALOG(R)File 348:EUROPEAN PATENTS

01021443
Dbpa, a helicase from Staphylococcus aureus
DbpA, eine Helikase aus Staphylococcus aureus
Dbpa, une helicase de Staphylococcus aureus
PATENT ASSIGNEE:
SMITHKLINE BEECHAM CORPORATION, (201244), One Franklin Plaza P.O. Box 7929, Philadelphia Pennsylvania 19103, (US), (Applicant designated States: all)
INVENTOR:
Huang, Jianzhong, Smithkline Beecham Pharmaceutic., 1250 South Collegeville Road, P.O. Box 5089, Collegeville, PA 19426-0989, (US)
McDevitt, Damien, Smithkline Beecham Pharmaceutic., 1250 South Collegeville Road, P.O. Box 5089, Collegeville, PA 19426-0989, (US)
Traini, Christopher M, Smithkline Beecham Pharmac., 1250 South Collegeville Road, P.O. Box 5089, Collegeville, PA 19426-0989, (US)
LEGAL REPRESENTATIVE:
Connell, Anthony Christopher et al (69941), SmithKline Beecham plc Corporate Intellectual Property, Two New Horizons Court, Brentford, Middlesex TW8 9EP, (GB)
PATENT (CC, No, Kind, Date): EP 913474 A2 990506 (Basic)
EP 913474 A3 991229
APPLICATION (CC, No, Date): EP 98203506 981019;
PRIORITY (CC, No, Date): US 958890 971028
DESIGNATED STATES: BE; CH; DE; DK; FR; GB; IT; LI; NL
EXTENDED DESIGNATED STATES: AL; LT; LV; MK; RO; SI
INTERNATIONAL PATENT CLASS: C12N-015/52; C12N-009/00; C07K-016/40; C12Q-001/68; G01N-033/566; A61K-048/00

ABSTRACT EP 913474 A2
The invention provides dbpA polypeptides and DNA (RNA) encoding dbpA polypeptides and methods for producing such polypeptides by recombinant techniques. Also provided are methods for utilizing dbpA polypeptides to *screen"** for antibacterial compounds.
ABSTRACT WORD COUNT: 34

LANGUAGE (Publication,Procedural,Application): English; English; English
FULLTEXT AVAILABILITY:

Available Text	Language	Update	Word Count
CLAIMS A	(English)	9918	607
SPEC A	(English)	9918	10487
Total word count - document A			11094
Total word count - document B			0
Total word count - documents A + B			11094

15/3,AB/54 (Item 2 from file: 348)
DIALOG(R)File 348:EUROPEAN PATENTS

01021429

Staphylococcus aureus member of the DEAD-type ATP-dependent RNA helicases (dbpB)
Staphylococcus aureus Mitglied der DEAD-type ATP-abhangigen RNA helicasen (dbpB)
Membre des RNA helicases ATP-dependantes de type DEAD (dbpB), de Staphylococcus aureus
PATENT ASSIGNEE:
SMITHKLINE BEECHAM CORPORATION, (201244), One Franklin Plaza P.O. Box 7929, Philadelphia Pennsylvania 19103, (US), (Applicant designated States: all)
INVENTOR:
Huang, Jianzhong, Smithkline Beecham Pharmaceutic., 1250 South Collegeville Road, P.O. Box 5089, Collegeville, PA 19426-0989, (US)
McDevitt, Damien, Smithkline Beecham Pharmaceutic., 1250 South Collegeville Road, P.O. Box 5089, Collegeville, PA 19426-0989, (US)
Wang, Min, Smithkline Beecham Pharmaceuticals, 1250 South Collegeville Road, P.O. Box 5089, Collegeville, PA 19426-0989, (US)
Traini, Christopher M., Smithkline Beech. Pharmac., 1250 South Collegeville Road, P.O. Box 5089, Collegeville, PA 19426-0989, (US)
LEGAL REPRESENTATIVE:
Mallalieu, Catherine Louise et al (69621), D. Young & Co., 21 New Fetter Lane, London EC4A 1DA, (GB)
PATENT (CC, No, Kind, Date): EP 913481 A2 990506 (Basic)
EP 913481 A3 991229
APPLICATION (CC, No, Date): EP 98203442 981012;
PRIORITY (CC, No, Date): US 959749 971028
DESIGNATED STATES: BE; CH; DE; DK; FR; GB; IT; LI; NL
EXTENDED DESIGNATED STATES: AL; LT; LV; MK; RO; SI
INTERNATIONAL PATENT CLASS: C12N-015/61; C12N-009/90; C12Q-001/533; C12Q-001/68; C07K-016/40; A61K-039/085; A61K-038/52; C12N-009/90; C12R-1:445

ABSTRACT EP 913481 A2
The invention provides dbpB polypeptides and DNA (RNA) encoding dbpB polypeptides and methods for producing such polypeptides by recombinant techniques. Also provided are methods for utilizing dbpB polypeptides to *screen"** for antibacterial compounds.
ABSTRACT WORD COUNT: 34

LANGUAGE (Publication,Procedural,Application): English; English; English
FULLTEXT AVAILABILITY:

Available Text	Language	Update	Word Count
CLAIMS A	(English)	9918	605
SPEC A	(English)	9918	10490
Total word count - document A			11095
Total word count - document B			0
Total word count - documents A + B			11095

15/3,AB/55 (Item 1 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

03506101 H.W. WILSON RECORD NUMBER: BGSA97006101
Bacterial diversity based on type II DNA topoisomerase genes.
Huang, Wai Mun
Annual Review of Genetics v. 30 (1996) p. 79-107
SPECIAL FEATURES: bibl il ISSN: 0066-4197

LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 11656

ABSTRACT: The use of type II DNA topoisomerases in studies of bacterial diversity and physiology is reviewed. Topoisomerases are ubiquitous in living cells, where they are essential for dealing with DNA topological problems. Eubacteria possess 2 essential and homologous type II topoisomerases: DNA gyrase, encoded by gyrA and gyrB, and topoisomerase IV, encoded by parE and parC. N-terminal regions of gyrA and parC have proved effective sequences for microbial identification and diversity analyses. In addition, the systematic and targeted generation of bacterial type II DNA topoisomerase gene sequences offers an opportunity for biochemical and structural studies of this gene family. Such studies have broad implications in DNA topology, DNA enzymology, and DNA metabolism.

15/3,AB/56 (Item 1 from file: 453)
DIALOG(R)File 453:Drugs of the Future

00265173 (Structure Image Available)
ENTRY NUMBER: 265173 (Actively Investigated)
DRUG NAME: ABT-773
A-195773.0
CHEM NAME: (1S,2R,5R,7R,8R,9R,11R,13R,14R)-2-Ethyl-1,5,7,9,11,13-hexamethyl-9-(3-(3-quinolyl)-2(E)-propenyloxy)-8-(3,4,6-trideoxy-3-(dimethylamino)-beta-D-glucopyranosyloxy)-3,17-dioxa-15-azabicyclo(12.3.0)heptadecane-4,12,16-trione
(3aS,4R,7R,9R,10R,11R,13R,15R,15aR)-4-Ethyl-3a,7,9,11,13,15-hexamethyl-11-(3-(3-quinolinyl)-2(E)-propenyloxy)-10-(3,4,6-trideoxy-3-(dimethylamino)-beta-D-xylo-hexopyranosyloxy)octahydro-2H-oxacyclotetradecino(4,3-d)oxazole-2,6,8,14(1H,7H,9H)-tetraone
11-Amino-11-deoxy-3-des(hexopyranosyloxy)-3-oxo-6-O-(3-(3-quinolinyl)-2(E)-propenyl)erythromycin A 11-N,12-O-cyclic carbamate
FORMULA: C42H59N3O10
CAS REG. NO.: 205110-48-1
DEVEL. PHASE: Phase III
ORIGINATOR: Abbott Labs.
Dainippon Pharmaceutical
Taisho
CLASS: 67000 (Antibiotics)
SYNTHESIS: 143400
127508

15/3,AB/57 (Item 2 from file: 453)
DIALOG(R)File 453:Drugs of the Future

00230662 (Structure Image Available)
ENTRY NUMBER: 230662
DRUG NAME: HMR-3647
RU-66647
GENERIC NAME Telithromycin (proposed INN)
BRAND NAME: Ketek (Aventis Pharma, , DE, ES, GB, IT, JP, MX, US, US)

	Levviax
CHEM NAME:	11-Deoxy-3-des(hexopyranosyloxy)-6-O-methyl-3-oxo-N-(4-(4-(3-pyridyl)imidazol-1-yl)butyl)amino erythromycin A 11-N,12-O-cyclic carbamate (3aS,4R,7R,9R,10R,11R,13R,15R,15aR)-4-Ethyl-11-methoxy-3a,7,9,11,13,15-hexamethyl-1-(4-(4-(3-pyridyl)imidazol-1-yl)butyl)-10-(3,4,6-trideoxy-3-(dimethylamino)-beta-D-xylo-hexopyranosyloxy)octahydro-2H-oxacyclotetradecino(4,3-d)oxazole-2,6,8,14(1H,7H,9H)-tetraone
FORMULA:	C43H65N5O10
CAS REG. NO.:	173838-31-8 191114-48-4 (RU-66647)
DEVEL. PHASE:	Launched (201901)
ORIGINATOR:	Aventis Pharma
CLASS:	67000 (Antibiotics)
SYNTHESIS:	65961

15/3,AB/58 (Item 3 from file: 453)
DIALOG(R)File 453:Drugs of the Future
(c) 2002 Prous Science. All rts. reserv.

00224298	(Structure Image Available)
ENTRY NUMBER:	224298
DRUG NAME:	PNU-100766 U-100766
GENERIC NAME	Linezolid (proposed INN; USAN)
BRAND NAME:	Zyvox (Pharmacia, GB, JP, US) Zyvoxa (Pharmacia, ES) Zyvoxam (Pharmacia, CA) Zyvoxid (Pharmacia,)
CHEM NAME:	N-(3-(3-Fluoro-4-(morpholin-4-yl)phenyl)-2-oxooxazolidin-5(S)-ylmethyl)acetamide
FORMULA:	C16H20FN3O4
CAS REG. NO.:	165800-03-3
DEVEL. PHASE:	Launched (201900)
ORIGINATOR:	Pharmacia
CLASS:	68000 (Antibacterial Drugs) 68241 (Oxazolidinones)
SYNTHESIS:	65843

15/3,AB/59 (Item 4 from file: 453)
DIALOG(R)File 453:Drugs of the Future
(c) 2002 Prous Science. All rts. reserv.

00121880	(Structure Image Available)
ENTRY NUMBER:	121880
DRUG NAME:	Abbott-56268 A-56268 TE-031
GENERIC NAME	Clarithromycin (recommended INN; BAN; USAN) 6-O-Methylerythromycin A
BRAND NAME:	Biaxin (Abbott Labs., US) Biaxin XL (Abbott Labs., US, US) Clarith (Taisho, JP) Cyllind (Abbott Labs., DE) Klacid (Abbott Labs., CH, DE, IE)

Klaricid (Abbott Labs., GB, GB;Dainabot, JP)
Klaricid XL (Abbott Labs., GB)
Macladin (Guidotti, IT)
Naxy (Sanofi-Synthelabo, FR, FR)
Veclam (Malesci, IT)

CHEM NAME: 6-O-Methylerythromycin
FORMULA: C38H69NO13
CAS REG. NO.: 81103-11-9
DEVEL. PHASE: Launched (201990)
ORIGINATOR: Sanofi-Synthelabo
Taisho
LICENSEE: Abbott Labs.
Dainabot
Guidotti
Malesci
CLASS: 54150 (Anti-Helicobacter Pylori Agents)
67000 (Antibiotics)
65000 (Macrolides)
SYNTHESIS: 02605
CONTEXT TABLE: 65000C (Macrolides)

15/3,AB/60 (Item 1 from file: 351)
DIALOG(R)File 351:Derwent WPI

012868513
WPI Acc No: 2000-040346/200004
XRAM Acc No: C00-010722
*Detecting"** *antibiotic"** *resistance"** in microorganisms by in situ characterization of probes
Patent Assignee: CREATOGEN BIOSCIENCES GMBH (CREA-N); CREATOGEN AG (CREA-N)
Inventor: APFEL H; HAAS R; TREBESIUS K
Number of Countries: 087 Number of Patents: 006
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
DE 19916610	A1	19991125	DE 1016610	A	19990413	200004	B
WO 9961660	A1	19991202	WO 99EP3527	A	19990521	200004	
AU 9942658	A	19991213	AU 9942658	A	19990521	200020	
BR 9910646	A	20010130	BR 9910646	A	19990521	200110	
			WO 99EP3527	A	19990521		
EP 1078104	A1	20010228	EP 99938039	A	19990521	200113	
			WO 99EP3527	A	19990521		
JP 2002516665	W	20020611	WO 99EP3527	A	19990521	200253	
			JP 2000551040	A	19990521		

Priority Applications (No Type Date): DE 1023098 A 19980522
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
DE 19916610	A1		28	C07H-021/00	
WO 9961660	A1	G		C12Q-001/68	

Designated States (National): AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW

AU 9942658	A	C12Q-001/68	Based on patent WO 9961660

BR 9910646 A C12Q-001/68 Based on patent WO 9961660
EP 1078104 A1 G C12Q-001/68 Based on patent WO 9961660
Designated States (Regional): AT BE CH DE DK ES FR GB IE IT LI NL SE
JP 2002516665 W 70 C12Q-001/68 Based on patent WO 9961660

Abstract (Basic): DE 19916610 A1
Abstract (Basic):
NOVELTY - *Detecting"** *antibiotic"** *resistance"** in microorganisms by in situ characterization of a probe hybridizing with an *antibiotic"** *resistance"** associated nucleic acid in a microorganism is new.
DETAILED DESCRIPTION - A method to *detect"** *antibiotic"** *resistance"** in microorganisms comprises the steps: preparing a microorganism containing test sample; contacting the sample with at least one hybridization probe, specific for an *antibiotic"** *resistance"** associated nucleic acid in the microorganism, under conditions specific for hybridization of the probe; evaluating the sample in situ through characterizing the appearance or failure of hybridization. INDEPENDENT CLAIMS are also included for: a reagent kit for typing microorganisms and/or *antibiotic"** *resistance"** in microorganisms through in situ hybridization; and oligonucleotides designated ClaR1, ClaR2, ClaR3, ClaWT, Hyp1-16S-753, 120b, Hyp1-16S-585 or Hyp1-16S-219 or that is at least 10 nucleotides in length and derived from these.
USE - The method is used to test slow growing and/or in vitro difficult or non cultivatable pathogens, e.g. *Helicobacter"** *pylori"**, Mycobacteria, Porphyromonas gigivalis, Propionibacterium acnes, Borrelia burgdorferi, Mycoplasma, Chlamydia, Tropheryma whippelii, Bartonella legionella, Norkardia and Actinomycetes. The sample can be prepared from human or animal tissue or body fluids. The method is used to test samples that have no previous preparation for the microorganism in question. In particular the method is used to *detect"** *antibiotic"** *resistance"** against in bacteria and protozoa.
pp; 28 DwgNo 0/1

15/3,AB/61 (Item 1 from file: 229)
DIALOG(R)File 229:Drug Info. Fulltext

00999927 AHFS NO: 08.12.12 AHFS CLASS: Macrolides
SUBFILE: AHFS Drug Information
MONOGRAPH TITLE: Azithromycin
GENERIC NAME: Azithromycin Dihydrate
CHEMICAL NAME: -beta-D-xylo-hexopyranosyloxy]-1-oxa-6-azacyclopentadecan-15-one; [2R-(2R,3S,4R,5R,8R,10R,11R,12S,13S,14R)]-13-[2,6,Dideoxy-3-C-methy l; -3-O-methyl-alpha-L-ribo-hexopyranosyl)oxy)-2-ethyl-3,4,10-trihydrox; y-3,5,6,8,10,12,14-heptamethyl-11-[[3,4,6,trideoxy-3-(dimethylamino); -beta -D-xylo-hexopyranosyloxy]-dihydrate
INVESTIGATIONAL NO: CP-62,993; XZ-450
BRAND NAME/MANUFACTURER: Zithromax Single Dose Packets/Pfizer; Zithromax Z-Pak/Pfizer; Zithromax/Pfizer
CAS REGISTRY NO: 83905-01-5; 117772-70-0
Subsections: 3224]_Pharyngitis and Tonsillitis; [3214]_Respiratory Tract Infections; [3224]_Otitis Media; [3224]_Skin and Skin Structure Infections; [3224]_Chlamydial Infections; [3226]_Urogenital Chlamydial Infections; [3226]_Presumptive Treatment of Chlamydial Infection in Patients with;

Gonorrhea; [3226]_Chlamydial Ophthalmia Neonatorum; [3226]_Other Chlamydial Infections; [3224]_Chancroid; [3224]_Gonorrhea; [3224]_Nongonococcal Urethritis; [3224]_Acute Pelvic Inflammatory Disease; [3224]_Mycobacterium avium Complex (MAC) Infections; [3226]_Primary Prevention of Disseminated MAC Infection; [3226]_Treatment and Secondary Prevention of Disseminated MAC; Infection; [3226]_Treatment of Pulmonary MAC Infections; [3224]_Prophylaxis of Bacterial Endocarditis; [3214]_Prophylaxis in Sexual Assault Victims; [3214]_*Helicobacter"** *pylori"** Infection; [3214]_Bartonella Infections; [3214]_Lyme Disease; [3214]_Toxoplasmosis; [3214]_Babesiosis; [3214]_Granuloma Inguinale (Donovanosis); [3214]_Cryptos poridiosis; [3574]_Reconstitution and Administration; [3576]_Oral Administration; [3456]_IV Infusion; [3524]_Dosage; [3506]_Adult Dosage; [3526]_Pharyngitis and Tonsillitis.; [3526]_Respiratory Tract Infections.; [3526]_Skin and Skin Structure Infections.; [3526]_Chlamydial Infections.; [3526]_Chancroid.; [3526]_Gonorrhea.; [3526]_Nongonococcal Urethritis.; [3526]_Acute Pelvic Inflammatory Disease.; [3526]_Primary Prevention of Disseminated Mycobacterium avium Complex; (MAC) Infections.; [3526]_Treatment and Secondary Prevention of Disseminated; Mycobacterium avium Complex (MAC) Infections.; [3526]_Treatment of Pulmonary Mycobacterium avium Complex (MAC); Infections.; [3526]_Prophylaxis of Bacterial Endocarditis.; [3526]_Prophylaxis in Sexual Assault Victims.; [3526]_Lyme Disease.; [3216]_Babesiosis.; [3506]_Pediatric Dosage; [3556]_Pharyngitis and Tonsillitis.; [3526]_Respiratory Tract Infections.; [3556]_Otitis Media.; [3526]_Chlamydial Infections.; [3526]_Chancroid.; [3526]_Primary Prevention of Disseminated Mycobacterium avium Complex; (MAC) Infections.; [3526]_Treatment and Secondary Prevention of Disseminated; Mycobacterium avium Complex (MAC) Infections.; [3526]_Prophylaxis of Bacterial Endocarditis.; [3556]_Lyme Disease.; [3216]_Babesiosis.; [3564]_Dosage in Renal and Hepatic Impairment; [3604]_GI Effects; [3604]_Dermatologic and Sensitivity Reactions; [3604]_Local Reactions; [3604]_Hepatic Effects; [3604]_Renal and Genitourinary Effects; [3604]_Cardiovascular Effects; [3604]_Nervous System Effects; [3604]_Hematologic Effects; [3604]_Otic Effects; [3604]_Other Adverse Effects; [3604]_Effects on Phospholipids; [3644]_Precautions and Contraindications; [3644]_Pediatric Precautions; [3644]_Geriatric Precautions; [3664]_*Mutagenicity"** and Carcinogenicity; [3654]_Pregnancy, Fertility, and Lactation; [3774]_Drugs Affecting Hepatic Microsomal Enzymes ; [3774]_Antacids; [3774]_Theophylline; [3774]_Nucleoside Reverse Transcriptase Inhibitors; [3774]_Rifabutin; [3774]_Warfarin; [3774]_Antilip emic Agents; [3774]_Cimetidine; [3774]_Midazolam; [3234]_In Vitro Susceptibility Testing; [3236]_Kirby-Bauer Disk-Diffusion Procedure; [3236]_Dilution Susceptibility Tests; [3274]_Gram-positive Aerobic Bacteria ; [3274]_Gram-negative Aerobic Bacteria; [3274]_Mycobacteria; [3274]_Anaerobic Bacteria; [3274]_Chlamydiae; [3274]_Mycoplasma; [3274]_Other Organisms; [3284]_Cross-resistance; [3814]_Absorption; [3824]_Distribution; [3834]_Elimination; [3104]_Chemistry; [3304]_Stability ; [3404]_Azithromycin

15/3,AB/62 (Item 1 from file: 444)
DIALOG(R)File 444:New England Journal of Med.

00122619

The Genetic Gymnastics of Our Indigenous Microbes (Clinical Implications of Basic Research)

Blaser, Martin J.
The New England Journal of Medicine
Jun 27, 2002; 346 (26),pp 2083-2085
LINE COUNT: 00144 WORD COUNT: 01987

Set	Items	Description
S16	6450	AU=(HAAS, R? OR HAAS R?)
S17	153	AU=(TREBESIUS, K? OR TREBESIUS K?)
S18	292	AU=(APFEL, H? OR APFEL H?)
S19	4	S16 AND S17 AND S18
S20	25	S16 AND (S17 OR S18)
S21	8	S17 AND S18
S22	6862	S16 OR S17 OR S18
S23	15	S22 AND S11
S24	27	(S19 OR S20 OR S21 OR S23) NOT S14
S25	11	RD (unique items)

- Author (s)

>>>No matching display code(s) found in file(s): 65, 129, 229, 453

25/3,AB/1 (Item 1 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

12598752 References: 24
TITLE: Specific detection and prevalence of Helicobacter heilmannii-like organisms in the human gastric mucosa by fluorescent in situ hybridization and partial 16S *ribosomal* DNA sequencing
AUTHOR(S): *Trebesius K"**; Adler K; Vieth M; Stolte M; *Haas R (REPRINT)"**
AUTHOR(S) E-MAIL: haas@m3401.mpk.med.uni-muenchen.de
CORPORATE SOURCE: Univ Munich, Max Von Pettenkofer Inst Hyg & Med Microbiol, Pettenkoferstr 9A/D-80336 Munich//Germany/ (REPRINT); Univ Munich, Max Von Pettenkofer Inst Hyg & Med Microbiol, /D-80336 Munich//Germany/; Klinikum Bayreuth, Inst Pathol, /Bayreuth//Germany/
PUBLICATION TYPE: JOURNAL
PUBLICATION: JOURNAL OF CLINICAL MICROBIOLOGY, 2001, V39, N4 (APR), P 1510-1516
GENUINE ARTICLE#: 419JX
PUBLISHER: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA
ISSN: 0095-1137
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: Gastric infection with Helicobacter heilmannii (previously known as Gastrospirillum hominis) is invariably linked with the presence of chronic gastritis and the risk of developing low-grade mucosa-associated lymphoid tissue lymphoma in humans. In contrast to Helicobacter pylori, various H. heilmannii species colonize the stomachs of domestic animals, which might be a reservoir for transmission to humans (zoonosis), To identify the number and prevalence of different H. heilmanni types in humans, we analyzed 89 gastric biopsy samples histologically identified as H. heilmannii positive by fluorescence in situ hybridization, Of these gastric specimens, 84 (94.4%) contained a single H. heilmannii type. In five samples, however, two different II. heilmannii types were detected, The most prevalent species in monoinfected samples is H. heilmannii type 1, found in 78.5% (66 of 84) of the specimens, followed by a novel H. heilmannii-like organism (HHLO), HHLO type 1, identified in 9.6% (8 of 84) of tissue sections, H. heilmannii type 2 and a further HHLO type not

described before, type 3, were found in 8.3% (7 of 84) and 1.2% (1 of 84) of the monoinfected samples, respectively. Additionally, HHLO type 5 with a 16S ribosomal DNA sequence identical to that of Helicobacter salomonis was found with a prevalence of 2.4% (2 of 89), Thirteen of these biopsy samples were also investigated by a PCR approach developed for this study that allows a Helicobacter-specific amplification of a variable portion of the 16S rRNA gene and subsequent sequencing. In total, five different types of HHLOs could be identified within these samples. We conclude that humans can be infected by at least five different HHLO types, which presumably have their origin in animal species like dogs, cats, and pigs.

25/3,AB/2 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

08091265 Genuine Article#: 234DN Number of References: 0
Title: Rapid and specific detection of Helicobacter pylori clarithromycin resistance genes in gastric tissue by fluorescent in situ hybridization
Author(s): *Trebesius K"**; Panthel K; Strobel S; Vogt K; Faller G; Kirchner T; Kist M; Heesemann J; *Haas R"**
Corporate Source: MAX VON PETTENKOFER INST HYG & MED MICROBIOL,/MUNICH//GERMANY/; DEPT MICROBIOL,/BERLIN//GERMANY/; INST MED MICROBIOL & HYG,/FREIBURG//GERMANY/; UNIV ERLANGEN NURNBERG,INST PATHOL/D-8520 ERLANGEN//GERMANY/; CREATOGEN BIOSCI GMBH,/AUGSBURG//GERMANY/
Journal: GUT, 1999, V45, 3 (SEP), PA123-A123
ISSN: 0017-5749 Publication date: 19990900
Publisher: BRITISH MED JOURNAL PUBL GROUP, BRITISH MED ASSOC HOUSE, TAVISTOCK SQUARE, LONDON WC1H 9JR, ENGLAND
Language: English Document Type: MEETING ABSTRACT

25/3,AB/3 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

13560033 BIOSIS NO.: 200200188854
Evaluation of a rapid fluorescent in situ hybridisation assay for detection of Helicobacter pylori and macrolide resistance in gastric biopsy samples.
AUTHOR: Birkner B(a); *Trebesius K"**; Adler K; Harmsen D; Thrippleton I; *Haas R"**
AUTHOR ADDRESS: (a)Gastroenterology Practice, Munich**Germany
JOURNAL: Abstracts of the General Meeting of the American Society for Microbiology 101p261 2001
MEDIUM: print
CONFERENCE/MEETING: 101st General Meeting of the American Society for Microbiology Orlando, FL, USA May 20-24, 2001
ISSN: 1060-2011
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: H. pylori causes chronic gastritis, predisposes to gastric and duodenal ulcers, and has been recognised as a gastric carcinogen. Histology of gastric biopsies is currently regarded as the "gold standard" to diagnose H. pylori infection. However, no resistance data are obtained by this and many other methods. For phenotypic resistance

determination, culture of H. pylori is necessary, which is time consuming and often unsuccessful. The development of macrolide resistance is, however, considered as the main reason for failure of antibiotic eradication therapy. To overcome this situation we recently developed a fluorescent in situ hybridisation (FISH) assay with probes directed against the rRNA for the rapid and specific genotypic detection of H. pylori and clarithromycin resistance in gastric tissue. Consequently, we performed a prospective study with 100 consecutive patients to evaluate the use of FISH. All patients were suffering from dyspepsia and two antrum biopsies were taken from each person. These specimens were sub sampled and analysed in parallel in a blinded manner by a pathologist (modified giemsa stain) and a microbiologist (culture, resistance phenotype by E-test, urease and FISH). According to the European guidelines for clinical trials, patients with at least two positive tests or with a positive culture only were classified as positive (n=32 cases). There was no significant (p=0.05) difference for discordant pairs between histology and FISH (McNemar chi-squared test, matched paired design). The results for resistance testing were in all cases concordant between E-test and FISH. However, in nine cases (28.1%) resistance testing was only possible by FISH. In conclusion, this new molecular method for the laboratory diagnosis of H. pylori is at least as reliable as histology with the substantial added value of macrolide resistance testing. FISH may thus, become an invaluable method especially in cases of therapy failures.

2001

25/3,AB/4 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

12477181 BIOSIS NO.: 200000230683
Rapid and specific detection of *Helicobacter"** *pylori"** macrolide resistance in gastric tissue by fluorescent in situ hybridisation.
AUTHOR: *Trebesius K"**; Panthel K; Strobel S; Vogt K; Faller G; Kirchner T ; Kist M; Heesemann J; *Haas R"**(a
AUTHOR ADDRESS: (a)Max von Pettenkofer Institute for Hygiene and Medical Microbiology, Pettenkoferstr. 9a, D-80336, Munich**Germany
JOURNAL: Gut 46 (5):p608-614 May, 2000
ISSN: 0017-5749
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: Background: The development of macrolide resistance in *Helicobacter"** *pylori"** is considered an essential reason for failure of antibiotic eradication therapies. The predominant mechanism of resistance to macrolides, particularly clarithromycin, is based on three defined mutations within *23S"** *rRNA"**, resulting in decreased binding of the antibiotic to the bacterial ribosome. Aim: To develop an rRNA based whole cell hybridisation method to detect *Helicobacter"** species in situ within gastric tissue, simultaneously with its clarithromycin resistance genotype. Methods: A set of fluorescent labelled oligonucleotide probes was developed, binding either to H *pylori"** 16S *rRNA"** or *23S"** *rRNA"** sequences containing specific point mutations responsible for clarithromycin resistance. After hybridisation

and stringent washing procedures, labelling of intact single bacteria was monitored by fluorescence microscopy. The new approach was compared with PCR based assays, histology, and microbiological culture. Results: In comparison with the phenotypic resistance measurement by E test, the genotypic clarithromycin resistance correlated perfectly (100%) for 35 H *pylori"** isolates analysed. In a set of gastric biopsy specimens (27) H *pylori"** infection was confirmed by histology (17/27) and correctly detected by whole cell hybridisation. Five clarithromycin resistant strains were identified in gastric tissue specimens directly. Furthermore, non-cultivable coccoid forms of H *pylori"** were easily detectable by whole cell hybridisation. Conclusions: Whole cell hybridisation of rRNA holds great promise for cultivation independent, reliable, and rapid (three hours) genotypic determination of clarithromycin resistance in H *pylori"**. Compared with PCR techniques it is independent of nucleic acid preparations, not prone to inhibition, and allows semi-quantitative visualisation of the bacteria within intact tissue samples.

2000

25/3,AB/5 (Item 1 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

136364347 CA: 136(24)364347h JOURNAL
Rapid and accurate determination of genotypic clarithromycin resistance in cultured Helicobacter pylori by fluorescent in situ hybridization
AUTHOR(S): Russmann, Holger; Adler, Kristin; Haas, Rainer; Gebert, Bettina; Koletzko, Sibylle; Heesemann, Jurgen
LOCATION: Max von Pettenkofer-Institut fur Hygiene und Medizinische Mikrobiologie, Ludwig Maximilians-Universitat Munchen, Munich, Germany, 80336
JOURNAL: J. Clin. Microbiol. DATE: 2001 VOLUME: 39 NUMBER: 11 PAGES: 4142-4144 CODEN: JCMIDW ISSN: 0095-1137 LANGUAGE: English PUBLISHER: American Society for Microbiology

25/3,AB/6 (Item 2 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

134363683 CA: 134(26)363683m PATENT
Determination of microorganisms in clinical and food samples by whole cell hybridization
INVENTOR(AUTHOR): Apfel, Heiko; Heesemann, Juergen; Trebesius, Karlheinz; Autenrieth, Ingo
LOCATION: Germany,
ASSIGNEE: Creatogen A.-G.
PATENT: PCT International ; WO 200136673 A2 DATE: 20010525
APPLICATION: WO 2000EP11386 (20001116) *DE 19955303 (19991117)
PAGES: 90 pp. CODEN: PIXXD2 LANGUAGE: German CLASS: C12Q-001/68A
DESIGNATED COUNTRIES: AE; AG; AL; AM; AT; AU; AZ; BA; BB; BG; BR; BY; BZ; CA; CH; CN; CR; CU; CZ; DE; DK; DM; DZ; EE; ES; FI; GB; GD; GE; GH; GM; HR; HU; ID; IL; IN; IS; JP; KE; KG; KP; KR; KZ; LC; LK; LR; LS; LT; LU; LV; MA; MD; MG; MK; MN; MW; MX; MZ; NO; NZ; PL; PT; RO; RU; SD; SE; SG; SI; SK; SL; TJ; TM; TR; TT; TZ; UA; UG; US; UZ; VN; YU; ZA; ZW; AM; AZ; BY; KG; KZ; MD; RU; TJ; TM DESIGNATED REGIONAL: GH; GM; KE; LS; MW; MZ; SD; SL; SZ; TZ; UG

; ZW; AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE; TR; BF; BJ; CF; CG; CI; CM; GA; GN; GW; ML; MR; NE; SN; TD; TG

25/3,AB/7 (Item 1 from file: 348)
DIALOG(R)File 348:EUROPEAN PATENTS

01304540
TEST FOR MICRO-ORGANISMS
TEST VON MIKROORGANISMEN
TEST POUR MICRO-ORGANISMES
PATENT ASSIGNEE:
Creatogen Aktiengesellschaft, (3189400), Ulmer Strasse 160a, 86156 Augsburg, (DE), (Applicant designated States: all)
INVENTOR:
*APFEL, Heiko"**, Ringstrasse 11a, 86356 Neusass, (DE)
HEESEMANN, Jurgen, Frickastrasse 12, 80639 Munchen, (DE)
*TREBESIUS, Karlheinz"**, Breitensteinstrasse 19, 83093 Bad Endorf, (DE)
AUTENRIETH, Ingo, Oberbiberger Strasse 50, 81547 Munchen, (DE
LEGAL REPRESENTATIVE:
Weiss, Wolfgang, Dipl.-Chem. Dr. et al (75611), Weickmann & Weickmann Patentanwalte Kopernikusstrasse 9, 81679 Munchen, (DE)
PATENT (CC, No, Kind, Date): EP 1232286 A2 020821 (Basic)
WO 2001036673 010525
APPLICATION (CC, No, Date): EP 2000985048 001116; WO 2000EP11386 001116
PRIORITY (CC, No, Date): DE 19955303 991117
DESIGNATED STATES: AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT; LI; LU; MC; NL; PT; SE; TR
EXTENDED DESIGNATED STATES: AL; LT; LV; MK; RO; SI
INTERNATIONAL PATENT CLASS: C12Q-001/68
NOTE:
No A-document published by EPO
LANGUAGE (Publication,Procedural,Application): German; German; German

25/3,AB/8 (Item 2 from file: 348)
DIALOG(R)File 348:EUROPEAN PATENTS

01114472
DEMONSTRATING RESISTANCE TO ANTIBIOTICS IN MICROORGANISMS
NACHWEIS VON ANTIBIOTIKUMRESISTENZEN IN MIKROORGANISMEN
MISE EN EVIDENCE DE RESISTANCES A DES ANTIBIOTIQUES DANS DES MICRO-ORGANISMES
PATENT ASSIGNEE:
Creatogen Aktiengesellschaft, (3189400), Ulmer Strasse 160a, 86156 Augsburg, (DE), (Applicant designated States: all)
INVENTOR:
*HAAS, Rainer"**, Weningstrasse 12, D-81547 Munchen, (DE)
*TREBESIUS, Karlheinz"**, Breitensteinstrasse 19, D-83093 Bad Endorf, (DE)
*APFEL, Heiko"**, Ringstrasse 11a, D-86356 Neusass, (DE
LEGAL REPRESENTATIVE:
Weiss, Wolfgang, Dipl.-Chem. Dr. et al (75611), Weickmann & Weickmann Patentanwalte Kopernikusstrasse 9, 81679 Munchen, (DE)
PATENT (CC, No, Kind, Date): EP 1078104 A1 010228 (Basic)
WO 9961660 991202

APPLICATION (CC, No, Date): EP 99938039 990521; WO 99EP3527 990521
PRIORITY (CC, No, Date): DE 19823098 980522; DE 19916610 990413
DESIGNATED STATES: AT; BE; CH; DE; DK; ES; FR; GB; IE; IT; LI; NL; SE
INTERNATIONAL PATENT CLASS: C12Q-001/68
NOTE:
No A-document published by EPO
LANGUAGE (Publication,Procedural,Application): German; German; German

25/3,AB/9 (Item 1 from file: 351)
DIALOG(R)File 351:Derwent WPI

013852413
WPI Acc No: 2001-336626/200136
XRAM Acc No: C01-104167
Direct and rapid identification of microorganisms, useful for determining pathogens that cause fulminant infections, based on hybridization with labeled immobilized probes
Patent Assignee: CREATOGEN AG (CREA-N)
Inventor: *APFEL H"**; AUTENRIETH I; HEESEMANN J; *TREBESIUS K"**
Number of Countries: 094 Number of Patents: 003
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
DE 19955303	A1	20010531	DE 1055303	A	19991117	200136	B
WO 200136673	A2	20010525	WO 2000EP11386	A	20001116	200138	
AU 200121598	A	20010530	AU 200121598	A	20001116	200152	

Priority Applications (No Type Date): DE 1055303 A 19991117
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
DE 19955303	A1		37	C07H-021/00	
WO 200136673	A2	G		C12Q-001/68	

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

AU 200121598	A			C12Q-001/68	Based on patent WO 200136673

Abstract (Basic): DE 19955303 A1
Abstract (Basic):

NOVELTY - Direct identification of microorganisms (A) in a biological sample comprises (i) dividing the sample into many parts (B); (ii) immobilizing (A) in (B); (iii) contacting (B) with at least one labeled hybridization probe (HP) and (iv) detecting bound label.

DETAILED DESCRIPTION - Direct identification of microorganisms (A) in a biological sample comprises (i) dividing the sample into many parts (B); (ii) immobilizing (A) in (B); (iii) contacting (B) with at least one labeled hybridization probe (HP) and (iv) detecting bound label. Different HP (or combinations of them) are used for each (B) and HP comprise a hybridization region that is complementary to a target sequence, available for hybridization within the cell, in (A)-specific nucleic acid.

INDEPENDENT CLAIMS are also included for:
(a) reagent kits for the process comprising a set of labeled HP;
(b) oligonucleotides (ON) containing, as region for hybridization

with a microbial target sequence, any of 34 listed sequence (or fragments of at least 10 nucleotides (nt) or sequences with at least 85 % identity); and

(c) a method for permeabilization of Gram-positive cells in a sample by treatment with lysozyme and lysostaphin.

USE - The method is used to identify (A), i.e. bacteria, fungi, protozoa or multi-cellular parasites, (i) in foods (or pharmaceuticals), for process or quality control and (ii) in clinical specimens, particularly for identifying pathogens associated with infections that need very quick diagnosis, especially septic shock, necrotizing fasciitis, sepsis, exacerbation of cystic fibrosis, urogenital infections during pregnancy, fulminant endocarditis, meningitis and ophthalmitis, but also for non-fulminant infections, e.g. tuberculosis, that requires quarantining of infected subjects.

ADVANTAGE - The method is sensitive, specific, simple (particularly no need for lysis, culturing or microscopy), produces reliable results in typically 3 hr, is relatively inexpensive, and can identify all potential pathogens associated with a particular disease. Compared with known in situ methods, sample sizes may be 10-20 times larger, increasing sensitivity by at least an order of magnitude. The method is suitable for routine use by non-expert personnel.

pp; 37 DwgNo 0/0

25/3,AB/10 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0272466 DBA Accession No.: 2001-11690 PATENT
Identification of microorganisms - using DNA probe for infection diagnosis and quality control
AUTHOR: *Apfel H"**; *Trebesius K"**; Autenrieth I; Heesemann J
CORPORATE SOURCE: Augsberg, Germany.
PATENT ASSIGNEE: Creatogen 2001
PATENT NUMBER: DE 19955303 PATENT DATE: 20010531 WPI ACCESSION NO.: 2001-336626 (2036)
PRIORITY APPLIC. NO.: DE 1055303 APPLIC. DATE: 19991117
NATIONAL APPLIC. NO.: DE 1055303 APPLIC. DATE: 19991117
LANGUAGE: German
ABSTRACT: Direct identification of microorganisms (A) in a biological sample by dividing the sample into many parts (B) immobilizing (A) in (B), contacting (B) with at least one hybridizable DNA probe and detecting bound label, is new. Also claimed are: reagent kits for the process containing a set of labeled DNA probes; oligonucleotides containing as region for hybridization with a microbial target sequence; and a method for permeabilization of Gram-positive cells in a sample by treatment with lysozyme and lysostaphin. The method is used to identify (A), i.e. bacteria, fungi, protozoa or multicellular parasites, in foods (or pharmaceuticals) for process or quality control and in clinical specimens, particularly for identifying pathogens associated with infections that need very quick diagnosis, especially septic shock, necrotizing fascitism sepsis, exacerbation of cystic fibrosis, urogenital infections during pregnancy, fulminant endocarditis, meningitis and ophthalmitis, but also for non-fulminant infections, e.g. tuberculosis, that requires quarantining of infected subjects. (37pp)

25/3,AB/11 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0248603 DBA Accession No.: 2000-03093 PATENT
Detecting antibiotic-resistance in microorganisms by in situ characterization of probes - hybridizing with an antibiotic-resistance associated nucleic acid
AUTHOR: *Haas R"**; *Trebesius K"**; *Apfel H"**
CORPORATE SOURCE: Augsburg, Germany.
PATENT ASSIGNEE: Creatogen-Biosciences 1999
PATENT NUMBER: DE 19916610 PATENT DATE: 19991125 WPI ACCESSION NO.: 2000-040346 (2004)
PRIORITY APPLIC. NO.: DE 1023098 APPLIC. DATE: 19980522
NATIONAL APPLIC. NO.: DE 1016610 APPLIC. DATE: 19990413
LANGUAGE: German
ABSTRACT: Detecting antibiotic resistance in microorganisms by in situ characterization of a probe hybridizing with an antibiotic-resistance associated nucleic acid in a microorganism is claimed. The method comprises: preparing a microorganisms containing test sample; contacting the sample with at least one hybridization DNA probe, specific for an antibiotic-resistance associated nucleic acid in the microorganism, under conditions specific for hybridization of the probe; and evaluating the sample in situ through characterizing the appearance of failure of hybridization. Also claimed are: a reagent kit for typing microorganisms and/or antibiotic-resistance in microorganisms through in situ hybridization; and oligonucleotides designated ClaR1, ClaR2, ClaR3, ClaWT, Hyp1-16s-753, 120b, Hyp1-16S-585 or Hyp1-16S-219 or that are at least 10 nucleotides in length and derived from these. The method is used to test slow growing and/or in vitro difficult or non cultivatable pathogens and to test samples that have no previous preparation for the microorganism and to detect antibiotic-resistant bacteria and protozoa. The sample can be prepared from human or animal tissue or body fluids. (28pp)
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;      NAME/KEY:  CDS
;      LOCATION:  1599..1847
US-08-852-865-1


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RESULT  26
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; Sequence 1, Application US/08876991
; Patent No. 5925360
;  GENERAL INFORMATION:
;    APPLICANT:  Gregor Meyers, Tillmann R menapf,
;    APPLICANT:  Heinz-J rgen Thiel
;    TITLE OF INVENTION:  Hog cholera virus vaccine and diagnostic
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Organon Teknika Corporation
;      ADDRESSEE:  Biotechnology Research Institute
;      STREET:  1330-A Piccard Drive
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  U.S.A.
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/876,991
;      FILING DATE:  16-JUN-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/747,577
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/650,584
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/469,702
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/123,596
;      FILING DATE:
;      APPLICATION NUMBER:  07/797,554
;      FILING DATE:  22-NOV-1991
;      APPLICATION NUMBER:  US 07/494,991
;      FILING DATE:  16-MAR-1990
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  William M. Blackstone
;      REGISTRATION NUMBER:  29,772
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 258-5200
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12284 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
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;    ORIGINAL SOURCE:
;      ORGANISM:  Hog cholera virus
;      STRAIN:  Alfort
;      CELL LINE:  PK 15  and 38A1D
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;      NAME/KEY:  primer_bind
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;      NAME/KEY:  variation
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US-08-876-991-1


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Db   1984 GGATCTTCCCGTCTT 1970


RESULT  27
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; Sequence 1, Application US/09059853
; Patent No. 5935582
;  GENERAL INFORMATION:
;    APPLICANT:  Gregor Meyers, Tillmann R menapf,
;    APPLICANT:  Heinz-J rgen Thiel
;    TITLE OF INVENTION:  Hog cholera virus vaccine and diagnostic
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Organon Teknika Corporation
;      ADDRESSEE:  Biotechnology Research Institute
;      STREET:  1330-A Piccard Drive
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  U.S.A.
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/059,853
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/797,554
;      FILING DATE:  22-NOV-1991
;      APPLICATION NUMBER:  US 07/494,991
;      FILING DATE:  16-MAR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  William M. Blackstone
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3876 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  579..3701
US-08-494-714-1


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RESULT  34
PCT-US96-10782-1
; Sequence 1, Application PC/TUS9610782
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University
;    APPLICANT:  of California
;    TITLE OF INVENTION:  STRESS TOLERANT YEAST MUTANTS
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROBBINS, BERLINER & CARSON
;      STREET:  201 N. Figueroa Street, 5th Floor
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90012-2628
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/10782
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berliner, Robert
;      REGISTRATION NUMBER:  20,121
;      REFERENCE/DOCKET NUMBER:  5555-400
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 977-1001
;      TELEFAX:  (213) 977-1003
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3876 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  579..3701
PCT-US96-10782-1


  Query Match             76.5%;  Score 13;  DB 5;  Length 3876;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ggggtcttcccgt 14
          |||||||||||||
Db   1666 GGGGTCTTCCCGT 1678


RESULT  35
US-08-390-878-18
; Sequence 18, Application US/08390878
; Patent No. 5700683
;  GENERAL INFORMATION:
;    APPLICANT:  Stover, Charles K.
;    APPLICANT:  Mahairas, Gregory G.
;    TITLE OF INVENTION:  VIRULENCE-ATTENUATING GENETIC DELETIONS
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Street Tower, 20th
;      STREET:  Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,878
;      FILING DATE:  17-FEB-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  15371A-17
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/543/9600
;      TELEFAX:  415/543/5043
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12412 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-390-878-18


  Query Match             76.5%;  Score 13;  DB 1;  Length 12412;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggtcttcccgtct 16
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Db    940 GGTCTTCCCGTCT 952


RESULT  36
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
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; GENERAL INFORMATION:
;  APPLICANT: Lindner, Luther E.
;  APPLICANT: Macphee, Kathleen
;  TITLE OF INVENTION: Human Blood Bacterium
;  FILE REFERENCE: D6026
;  CURRENT APPLICATION NUMBER: US/09/187,946
;  CURRENT FILING DATE: 1998-11-02
;  EARLIER APPLICATION NUMBER: US 60/064,472
;  EARLIER FILING DATE: 1997-11-06
;  NUMBER OF SEQ ID NOS: 20
; SEQ ID NO 4
;   LENGTH: 2061
;   TYPE: DNA
;   ORGANISM: unknown
;   FEATURE:
;   OTHER INFORMATION: 58 23S rRNA sequence of a new human blood bacterium
US-09-187-946-4


  Query Match             84.7%;  Score 14.4;  DB 4;  Length 2061;
  Best Local Similarity   93.8%;  Pred. No. 64;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtct 16
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Db    1865 CGGGGTCTTTCCGTCT 1850


RESULT   8
US-09-187-946-3/c
; Sequence 3, Application US/09187946
; Patent No. 6255467
; GENERAL INFORMATION:
;  APPLICANT: Lindner, Luther E.
;  APPLICANT: Macphee, Kathleen
;  TITLE OF INVENTION: Human Blood Bacterium
;  FILE REFERENCE: D6026
;  CURRENT APPLICATION NUMBER: US/09/187,946
;  CURRENT FILING DATE: 1998-11-02
;  EARLIER APPLICATION NUMBER: US 60/064,472
;  EARLIER FILING DATE: 1997-11-06
;  NUMBER OF SEQ ID NOS: 20
; SEQ ID NO 3
;   LENGTH: 2542
;   TYPE: DNA
;   ORGANISM: unknown
;   FEATURE:
;   OTHER INFORMATION: Rb 23S rRNA sequence of a new human blood bacterium
US-09-187-946-3


  Query Match             84.7%;  Score 14.4;  DB 4;  Length 2542;
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Qy       1 cggggtcttcccgtct 16
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Db    1867 CGGGGTCTTTCCGTCT 1852


RESULT   9
US-08-746-111-4/c
; Sequence 4, Application US/08746111
; Patent No. 6066778
;  GENERAL INFORMATION:
;    APPLICANT:  Ginsburg, David
;    APPLICANT:  Cui, Jisong
;    TITLE OF INVENTION:  Compositions And Methods For Screening
;    TITLE OF INVENTION:  Compounds For Anticoagulant Activity
;    NUMBER OF SEQUENCES:  54
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/746,111
;      FILING DATE:  06-NOV-1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  UM-02536
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6585 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "DNA"
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  6..6554
US-08-746-111-4


  Query Match             84.7%;  Score 14.4;  DB 3;  Length 6585;
  Best Local Similarity   93.8%;  Pred. No. 69;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ggggtcttcccgtctt 17
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Db    2619 GGGGTCTTCCTGTCTT 2604


RESULT  10
US-09-398-193-98
; Sequence 98, Application US/09398193
; Patent No. 6197581
; GENERAL INFORMATION:
;  APPLICANT: Medical Research Council
;  TITLE OF INVENTION: Adenylate cyclase and uses therefor
;  FILE REFERENCE: P24360-
;  CURRENT APPLICATION NUMBER: US/09/398,193
;  CURRENT FILING DATE: 1999-09-17
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
;   LENGTH: 5515
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (539)..(4600)
US-09-398-193-98


  Query Match             82.4%;  Score 14;  DB 4;  Length 5515;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 ggggtcttcccgtc 15
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Db    5387 ggggtcttcccgtc 5400
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US-08-778-656-3

Query Match 90.6%; Score 15.4; DB 2; Length 3625;
Best Local Similarity 94.1%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||||||| ||||
Db 1491 CGGGGTCTTCCCATCTT 1475

RESULT 5
US-08-356-354-1/c
; Sequence 1, Application US/08356354
; Patent No. 5767365
; GENERAL INFORMATION:
; APPLICANT: SONNEWALD, Uwe
; TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE
; TITLE OF INVENTION: PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,354
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/EP93/01605
; FILING DATE: 22-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P42 20 758.4
; FILING DATE: 24-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meilman, Edward A.
; REGISTRATION NUMBER: 24,735
; REFERENCE/DOCKET NUMBER: P/951-105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 382-0700
; TELEFAX: (212) 382-0888
; TELEX: 236925
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3740 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Solanum tuberosum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 957..3494
; OTHER INFORMATION: /note= "Sucrose-Phosphate-Synthase"
US-08-356-354-1

Query Match 90.6%; Score 15.4; DB 1; Length 3740;
Best Local Similarity 94.1%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
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Db 1703 CGGGGTCTTCCCATCTT 1687

RESULT 6
US-08-778-656-1/c
; Sequence 1, Application US/08778656
; Patent No. 5976869
; GENERAL INFORMATION:
; APPLICANT: SONNEWALD, Uwe
; TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE
; TITLE OF INVENTION: PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/778,656
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/356,354
; FILING DATE: 20-DEC-1994
; APPLICATION NUMBER: US PCT/EP93/01605
; FILING DATE: 22-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P42 20 758.4
; FILING DATE: 24-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meilman, Edward A.
; REGISTRATION NUMBER: 24,735
; REFERENCE/DOCKET NUMBER: P/951-105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 382-0700
; TELEFAX: (212) 382-0888
; TELEX: 236925
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3740 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Solanum tuberosum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 957..3494
; OTHER INFORMATION: /note= "Sucrose-Phosphate-Synthase"
US-08-778-656-1

Query Match 90.6%; Score 15.4; DB 2; Length 3740;
Best Local Similarity 94.1%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
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Db 1703 CGGGGTCTTCCCATCTT 1687

RESULT 7
US-09-187-946-4/c
; Sequence 4, Application US/09187946
; Patent No. 6255467

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;  PRIOR APPLICATION NUMBER: US 09/325,601
;  PRIOR FILING DATE: 1999-06-03
;  PRIOR APPLICATION NUMBER: GB 9812196.5
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: GB 9904790.4
;  PRIOR FILING DATE: 1999-03-02
;  PRIOR APPLICATION NUMBER: US 60/122,439
;  PRIOR FILING DATE: 1999-03-02
;  PRIOR APPLICATION NUMBER: US 60/088,241
;  PRIOR FILING DATE: 1998-06-05
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 2904
;   TYPE: RNA
;   ORGANISM: Escherichia coli
US-09-465-355-3


  Query Match             90.6%;  Score 15.4;  DB 4;  Length 2904;
  Best Local Similarity   94.1%;  Pred. No. 20;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
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Db   2068 CGGGGTCTTTCCGTCTT 2052


RESULT   3
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; Sequence 3, Application US/08356354
; Patent No. 5767365
;  GENERAL INFORMATION:
;    APPLICANT:  SONNEWALD, Uwe
;    TITLE OF INVENTION:  DNA SEQUENCES AND PLASMIDS FOR THE
;    TITLE OF INVENTION:  PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ostrolenk, Faber, Gerb & Soffen
;      STREET:  1180 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  US
;      ZIP:  10036-8403
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/356,354
;      FILING DATE:  20-DEC-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US PCT/EP93/01605
;      FILING DATE:  22-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P42 20 758.4
;      FILING DATE:  24-JUN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meilman, Edward A.
;      REGISTRATION NUMBER:  24,735
;      REFERENCE/DOCKET NUMBER:  P/951-105
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 382-0700
;      TELEFAX:  (212) 382-0888
;      TELEX:  236925
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3625 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Solanum tuberosum
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  121..3282
;      OTHER INFORMATION:  /note= "Sucrose-Phosphate-Synthase"
US-08-356-354-3


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  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
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Db   1491 CGGGGTCTTCCCATCTT 1475


RESULT   4
US-08-778-656-3/c
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; Patent No. 5976869
;  GENERAL INFORMATION:
;    APPLICANT:  SONNEWALD, Uwe
;    TITLE OF INVENTION:  DNA SEQUENCES AND PLASMIDS FOR THE
;    TITLE OF INVENTION:  PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ostrolenk, Faber, Gerb & Soffen
;      STREET:  1180 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  US
;      ZIP:  10036-8403
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/778,656
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/356,354
;      FILING DATE:  20-DEC-1994
;      APPLICATION NUMBER:  US PCT/EP93/01605
;      FILING DATE:  22-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P42 20 758.4
;      FILING DATE:  24-JUN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meilman, Edward A.
;      REGISTRATION NUMBER:  24,735
;      REFERENCE/DOCKET NUMBER:  P/951-105
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 382-0700
;      TELEFAX:  (212) 382-0888
;      TELEX:  236925
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3625 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Solanum tuberosum
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  121..3282
;      OTHER INFORMATION:  /note= "Sucrose-Phosphate-Synthase"
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 17:46:20 ; Search time 65.61 Seconds
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Title: US-09-673-645A-1
Perfect score: 17
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Listing first 50 summaries

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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	15.4	90.6	86	4	US-09-565-596-13	Sequence 13, Appl
c 2	15.4	90.6	2904	4	US-09-465-355-3	Sequence 3, Appli
c 3	15.4	90.6	3625	1	US-08-356-354-3	Sequence 3, Appli
c 4	15.4	90.6	3625	2	US-08-778-656-3	Sequence 3, Appli
c 5	15.4	90.6	3740	1	US-08-356-354-1	Sequence 1, Appli
c 6	15.4	90.6	3740	2	US-08-778-656-1	Sequence 1, Appli
c 7	14.4	84.7	2061	4	US-09-187-946-4	Sequence 4, Appli
c 8	14.4	84.7	2542	4	US-09-187-946-3	Sequence 3, Appli
c 9	14.4	84.7	6585	3	US-08-746-111-4	Sequence 4, Appli
10	14	82.4	5515	4	US-09-398-193-98	Sequence 98, Appl
c 11	13.8	81.2	85	4	US-09-565-596-14	Sequence 14, Appl
c 12	13.8	81.2	86	4	US-09-565-596-12	Sequence 12, Appl
c 13	13.8	81.2	86	4	US-09-565-596-17	Sequence 17, Appl
c 14	13.8	81.2	1869	2	US-08-371-377-21	Sequence 21, Appl
c 15	13.8	81.2	2930	1	US-08-356-354-5	Sequence 5, Appli
c 16	13.8	81.2	2930	2	US-08-778-656-5	Sequence 5, Appli
17	13.8	81.2	4403765	4	US-09-103-840A-2	Sequence 2, Appli
18	13.4	78.8	59	4	US-09-626-929-7	Sequence 7, Appli
c 19	13.4	78.8	350	3	US-08-888-077A-32	Sequence 32, Appl
c 20	13.4	78.8	1035	3	US-08-733-837B-1	Sequence 1, Appli
c 21	13.4	78.8	2564	1	US-08-224-983-1	Sequence 1, Appli
c 22	13.4	78.8	2564	2	US-08-852-933-1	Sequence 1, Appli
c 23	13.4	78.8	2564	2	US-08-852-945-1	Sequence 1, Appli
c 24	13.4	78.8	2564	2	US-08-853-021-1	Sequence 1, Appli
c 25	13.4	78.8	2564	3	US-08-852-865-1	Sequence 1, Appli
c 26	13.4	78.8	12284	2	US-08-876-991-1	Sequence 1, Appli
c 27	13.4	78.8	12284	2	US-09-059-853-1	Sequence 1, Appli
c 28	13.4	78.8	16569	4	US-09-097-889-2	Sequence 2, Appli
c 29	13.4	78.8	16569	4	US-09-377-856-1	Sequence 1, Appli
c 30	13.4	78.8	17710	4	US-08-976-259-70	Sequence 70, Appl
31	13.4	78.8	176373	3	US-09-128-155-17	Sequence 17, Appl
c 32	13	76.5	690	4	US-08-861-774E-77	Sequence 77, Appl
33	13	76.5	3876	1	US-08-494-714-1	Sequence 1, Appli
34	13	76.5	3876	5	PCT-US96-10782-1	Sequence 1, Appli
35	13	76.5	12412	1	US-08-390-878-18	Sequence 18, Appl
c 36	13	76.5	4411529	4	US-09-103-840A-1	Sequence 1, Appli
c 37	12.8	75.3	52	4	US-09-091-814-34	Sequence 34, Appl
38	12.8	75.3	195	1	US-08-466-033-92	Sequence 92, Appl
39	12.8	75.3	195	1	US-08-444-733-92	Sequence 92, Appl
40	12.8	75.3	195	2	US-08-464-134-92	Sequence 92, Appl
41	12.8	75.3	195	2	US-08-461-361-92	Sequence 92, Appl
42	12.8	75.3	195	2	US-08-485-910-92	Sequence 92, Appl
43	12.8	75.3	195	5	PCT-US95-06266-76	Sequence 76, Appl
44	12.8	75.3	203	1	US-08-466-033-19	Sequence 19, Appl
45	12.8	75.3	203	1	US-08-444-733-19	Sequence 19, Appl
46	12.8	75.3	203	2	US-08-464-134-19	Sequence 19, Appl
47	12.8	75.3	203	2	US-08-461-361-19	Sequence 19, Appl
48	12.8	75.3	203	2	US-08-485-910-19	Sequence 19, Appl
49	12.8	75.3	203	5	PCT-US95-06266-19	Sequence 19, Appl
50	12.8	75.3	237	1	US-08-466-033-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-565-596-13/c
; Sequence 13, Application US/09565596
; Patent No. 6235484
; GENERAL INFORMATION:
; APPLICANT: Hogan, James J.
; APPLICANT: Gordon, Patricia
; TITLE OF INVENTION: Polynucleotide Probes for Detection and
; TITLE OF INVENTION: Quantitation of Actinomycetes
; FILE REFERENCE: GP109-02.UT
; CURRENT APPLICATION NUMBER: US/09/565,596
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,412
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 86
; TYPE: RNA
; ORGANISM: E. coli
US-09-565-596-13

Query Match 90.6%; Score 15.4; DB 4; Length 86;
Best Local Similarity 94.1%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
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Db 85 CGGGGTCTTTCCGTCTT 69

RESULT 2
US-09-465-355-3/c
; Sequence 3, Application US/09465355
; Patent No. 6316194
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; APPLICANT: Knowles, David
; APPLICANT: Murchie, Alastair
; APPLICANT: Lentzen, Georg
; TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Antimicrobials
; FILE REFERENCE: 22620/1150 (Formerly 3950/85276)
; CURRENT APPLICATION NUMBER: US/09/465,355
; CURRENT FILING DATE: 1999-12-16

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 17:41:45 ; Search time 1830.23 Seconds
(without alignments)
194.375 Million cell updates/sec

Title: US-09-673-645A-1
Perfect score: 17
Sequence: 1 cggggtcttcccgtctt 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
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6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description
	1	17	100.0	17	6	AX009453	AX009453 Sequence
c	2	17	100.0	178	1	AB041501	AB041501 Helicobac
c	3	16	94.1	692	1	AF200365	AF200365 Treponema
	4	15.4	90.6	17	6	AX009455	AX009455 Sequence
	5	15.4	90.6	17	6	AX009456	AX009456 Sequence
c	6	15.4	90.6	86	6	AR153334	AR153334 Sequence
c	7	15.4	90.6	86	6	AX045402	AX045402 Sequence
c	8	15.4	90.6	102	1	ECORRG22	K01128 E.coli 23S
c	9	15.4	90.6	178	1	AB041500	AB041500 Helicobac
c	10	15.4	90.6	372	5	GONSP16SR	X86060 Gonatodes s
c	11	15.4	90.6	387	3	AB020407	AB020407 Fasciola
c	12	15.4	90.6	391	3	AB020409	AB020409 Schistoso
c	13	15.4	90.6	400	3	AF122971	AF122971 Cerastode
c	14	15.4	90.6	405	5	MTLARNA16	Z46487 L.albirostr
c	15	15.4	90.6	420	5	AB028789	AB028789 Mabuya qu
c	16	15.4	90.6	421	5	AB028791	AB028791 Mabuya st
c	17	15.4	90.6	427	5	MTALIM16S	Z48657 A.limifrons
c	18	15.4	90.6	436	5	LCU39982	U39982 Litoria cyc
c	19	15.4	90.6	439	3	AF122972	AF122972 Cerastode
c	20	15.4	90.6	441	3	AF152022	AF152022 Corbicula
c	21	15.4	90.6	442	3	AF152024	AF152024 Corbicula
c	22	15.4	90.6	443	3	AF152023	AF152023 Corbicula
c	23	15.4	90.6	451	5	SEOMTRGAJ	L41479 Sceloporus
c	24	15.4	90.6	455	5	SCAF000830	AF000830 Sceloporu
c	25	15.4	90.6	457	3	AF038999	AF038999 Corbicula
c	26	15.4	90.6	457	5	SSAF000868	AF000868 Sceloporu
c	27	15.4	90.6	459	3	CGL243574	AJ243574 Chlamys g
c	28	15.4	90.6	459	5	AF113638	AF113638 Hydromedu
c	29	15.4	90.6	482	3	AF360118	AF360118 Carybdea
c	30	15.4	90.6	487	3	ACO243882	AJ243882 Adamussiu
c	31	15.4	90.6	490	5	AF153560	AF153560 Mabuya ac
c	32	15.4	90.6	490	5	AF153562	AF153562 Mabuya bi
c	33	15.4	90.6	504	5	AF153569	AF153569 Mabuya ho
c	34	15.4	90.6	504	5	AF153571	AF153571 Mabuya ir
c	35	15.4	90.6	504	5	AF153575	AF153575 Mabuya ma
c	36	15.4	90.6	504	5	AF153579	AF153579 Mabuya qu
c	37	15.4	90.6	504	5	AF153584	AF153584 Mabuya va
c	38	15.4	90.6	505	5	AF153564	AF153564 Mabuya ca
c	39	15.4	90.6	505	5	AF153578	AF153578 Mabuya pe
c	40	15.4	90.6	505	5	AF153580	AF153580 Mabuya sp
c	41	15.4	90.6	506	5	AF153565	AF153565 Mabuya co
c	42	15.4	90.6	506	5	AF153574	AF153574 Mabuya ma
c	43	15.4	90.6	506	5	AF153577	AF153577 Mabuya oc
c	44	15.4	90.6	507	5	AF153570	AF153570 Mabuya ho
c	45	15.4	90.6	507	5	AF153585	AF153585 Mabuya va
c	46	15.4	90.6	508	5	AF153566	AF153566 Mabuya cf
c	47	15.4	90.6	508	5	AF153568	AF153568 Mabuya el
c	48	15.4	90.6	508	5	AF153581	AF153581 Mabuya st
c	49	15.4	90.6	508	5	AF153583	AF153583 Mabuya su
c	50	15.4	90.6	509	5	AF153567	AF153567 Mabuya el

ALIGNMENTS

RESULT 1
AX009453
LOCUS AX009453 17 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 1 from Patent WO9961660.
ACCESSION AX009453
VERSION AX009453.1 GI:9996739
KEYWORDS .
SOURCE Helicobacter pylori.
ORGANISM Helicobacter pylori
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
REFERENCE 1 (bases 1 to 17)
AUTHORS Trebesius,K., Apfel,H. and Haas,R.
TITLE Demonstrating resistance to antibiotics in microorganisms
JOURNAL Patent: WO 9961660-A 1 02-DEC-1999;
TREBESIUS KARLHEINZ (DE); APFEL HEIKO (DE); HAAS RAINER (DE);
CREATOGEN BIOSCIENCES GMBH (DE)
FEATURES Location/Qualifiers

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     source          1. .17
                     /organism="Helicobacter pylori"
                     /db_xref="taxon:210"
                     /note="A2058G (ClaR)"
BASE COUNT        0 a      6 c      5 g      6 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          |||||||||||||||||
Db      1 CGGGGTCTTCCCGTCTT 17


RESULT   2
AB041501/c
LOCUS       AB041501                 178 bp    DNA     linear   BCT 18-APR-2000
DEFINITION  Helicobacter pylori gene for 23S rRNA, partial sequence,
            strain:MHP-002.
ACCESSION   AB041501
VERSION     AB041501.1  GI:7576351
KEYWORDS    .
SOURCE      Helicobacter pylori (strain:MHP-002) DNA.
  ORGANISM  Helicobacter pylori
            Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
            Helicobacter.
REFERENCE   1  (bases 1 to 178)
  AUTHORS   Takayama,S. and Suga,M.
  TITLE     Partial nucleotide sequence of the 23S rRNA gene of H.pylori
  JOURNAL   Published Only in DataBase (2000) In press
REFERENCE   2  (bases 1 to 178)
  AUTHORS   Takayama,S. and Suga,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-APR-2000) to the DDBJ/EMBL/GenBank databases.
            Shigenobu Takayama, St Marianna University Yokohamashi Seibu
            Hospital, Division of Laboratory Research; 1197-1 Yazashi Asahiku,
            Yokohama, Kanagawa 241-0811, Japan (E-mail:stakayam@mb.kcom.ne.jp,
            Tel:81-45-366-1111(ex.3352), Fax:81-45-366-1190)
FEATURES             Location/Qualifiers
     source          1. .178
                     /organism="Helicobacter pylori"
                     /strain="MHP-002"
                     /db_xref="taxon:210"
                     /note="isolate with the point mutation of A2143G on the
                     23S rRNA gene from a patient who failed the eradication
                     therapy by the treatment with AMPC, CAM and PPI."
     rRNA            <1. .>178
                     /product="23S ribosomal RNA"
BASE COUNT       47 a     40 c     50 g     41 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          |||||||||||||||||
Db     80 CGGGGTCTTCCCGTCTT 64


RESULT   3
AF200365/c
LOCUS       AF200365                 692 bp    DNA     linear   BCT 29-FEB-2000
DEFINITION  Treponema pallidum subsp. pallidum strain Street strain 14 23S
            ribosomal RNA gene, partial sequence.
ACCESSION   AF200365
VERSION     AF200365.1  GI:7108947
KEYWORDS    .
SOURCE      syphilis treponeme.
  ORGANISM  Treponema pallidum subsp. pallidum
            Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
REFERENCE   1  (bases 1 to 692)
  AUTHORS   Stamm,L.V. and Bergen,H.L.
  TITLE     A point mutation associated with bacterial macrolide resistance is
            present in both 23S rRNA genes of an erythromycin-resistant
            Treponema pallidum clinical isolate
  JOURNAL   Antimicrob. Agents Chemother. 44 (3), 806-807 (2000)
  MEDLINE   20210540
REFERENCE   2  (bases 1 to 692)
  AUTHORS   Stamm,L.V. and Bergen,H.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-1999) Department of Epidemiology, University of
            North Carolina at Chapel Hill, CB# 7400 2107 McGavran-Greenberg,
            Chapel Hill, NC 27599-7400, USA
FEATURES             Location/Qualifiers
     source          1. .692
                     /organism="Treponema pallidum subsp. pallidum"
                     /strain="Street strain 14"
                     /db_xref="taxon:161"
     rRNA            <1. .>692
                     /note="sequences of both the 23S rRNA genes are identical
                     in this region"
                     /product="23S ribosomal RNA"
BASE COUNT      166 a    156 c    216 g    154 t
ORIGIN


  Query Match             94.1%;  Score 16;  DB 1;  Length 692;
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  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtct 16
          ||||||||||||||||
Db    143 CGGGGTCTTCCCGTCT 128


RESULT   4
AX009455
LOCUS       AX009455                 17 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 3 from Patent WO9961660.
ACCESSION   AX009455
VERSION     AX009455.1  GI:9996741
KEYWORDS    .
SOURCE      Helicobacter pylori.
  ORGANISM  Helicobacter pylori
            Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
            Helicobacter.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Trebesius,K., Apfel,H. and Haas,R.
  TITLE     Demonstrating resistance to antibiotics in microorganisms
  JOURNAL   Patent: WO 9961660-A 3 02-DEC-1999;
            TREBESIUS KARLHEINZ (DE); APFEL HEIKO (DE); HAAS RAINER (DE);
            CREATOGEN BIOSCIENCES GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Helicobacter pylori"
                     /db_xref="taxon:210"
                     /note="A2058C (ClaR)"
BASE COUNT        0 a      5 c      6 g      6 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 6;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db      1 CGGGGTCTTGCCGTCTT 17


RESULT   5
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AX009456
LOCUS       AX009456                17 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 4 from Patent WO9961660.
ACCESSION   AX009456
VERSION     AX009456.1  GI:9996742
KEYWORDS    .
SOURCE      Helicobacter pylori.
  ORGANISM  Helicobacter pylori
            Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
            Helicobacter.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Trebesius,K., Apfel,H. and Haas,R.
  TITLE     Demonstrating resistance to antibiotics in microorganisms
  JOURNAL   Patent: WO 9961660-A 4 02-DEC-1999;
            TREBESIUS KARLHEINZ (DE); APFEL HEIKO (DE); HAAS RAINER (DE);
            CREATOGEN BIOSCIENCES GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Helicobacter pylori"
                     /db_xref="taxon:210"
                     /note="Wildtyp"
BASE COUNT        0 a      5 c      5 g      7 t
ORIGIN


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  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db      1 CGGGGTCTTTCCGTCTT 17


RESULT   6
AR153334/c
LOCUS       AR153334                86 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 13 from patent US 6235484.
ACCESSION   AR153334
VERSION     AR153334.1  GI:15120866
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 86)
  AUTHORS   Hogan,J.J. and Gordon,P.
  TITLE     Polynucleotide probes for detection and quantitation of
            actinomycetes
  JOURNAL   Patent: US 6235484-A 13 22-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .86
                     /organism="unknown"
BASE COUNT       22 a     25 c     25 g     14 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 6;  Length 86;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db     85 CGGGGTCTTTCCGTCTT 69


RESULT   7
AX045402/c
LOCUS       AX045402                86 bp    mRNA    linear   PAT 24-NOV-2000
DEFINITION  Sequence 13 from Patent WO0066786.
ACCESSION   AX045402
VERSION     AX045402.1  GI:11343886
KEYWORDS    .
SOURCE      Escherichia coli.
  ORGANISM  Escherichia coli
            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
            Escherichia.
REFERENCE   1  (bases 1 to 86)
  AUTHORS   Hogan,J.J. and Gordon,P.
  TITLE     Polynucleotide probes for detection and quantitation of
            actinomycetes
  JOURNAL   Patent: WO 0066786-A 13 09-NOV-2000;
            Gen-Probe Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .86
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     misc_feature    1. .86
                     /note="Segment of rRNA"
BASE COUNT       22 a     25 c     25 g     14 t
ORIGIN


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  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db     85 CGGGGTCTTTCCGTCTT 69


RESULT   8
ECORRG22/c
LOCUS       ECORRG22                102 bp    rRNA    linear   BCT 11-AUG-1995
DEFINITION  E.coli 23S ribosomal RNA, fragment S/T.
ACCESSION   K01128
VERSION     K01128.1  GI:174403
KEYWORDS    23S ribosomal RNA; L1 protein; binding site; ribosomal RNA.
SEGMENT     22 of 26
SOURCE      Escherichia coli (strain MRE 600 [1]) rRNA.
  ORGANISM  Escherichia coli
            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
            Escherichia.
REFERENCE   1  (bases 63 to 102)
  AUTHORS   Branlant,C., Korobko,V. and Ebel,J.P.
  TITLE     The binding site of protein L1 on 23-S ribosomal RNA from
            Escherichia coli. 3.Nucleotide sequence
  JOURNAL   Eur. J. Biochem. 70 (2), 471-482 (1976)
  MEDLINE   77091027
REFERENCE   2  (bases 1 to 102)
  AUTHORS   Branlant,C., Krol,A., Machatt,M.A. and Ebel,J.P.
  TITLE     Structural study of ribosomal 23 S RNA from Escherichia coli
  JOURNAL   FEBS Lett. 107 (1), 177-181 (1979)
  MEDLINE   80047286
COMMENT     [1]  see comment.
            See segment 1. [1] shows the almost complete sequence of a region
            of the 23S rRNA containing the L1 protein binding site, and
            suggests possible secondary structure models. The sequence is 175
            bp in length. [1] proposes that it is located between the 550th and
            1000th nucleotide at the 3' end of the 23S RNA. Comparison between
            [1] and [2] sequence data, however, shows very little homology, the
            most homologous region being between bases 63 and 102 of this
            segment. Given sequence is that of [2].
FEATURES             Location/Qualifiers
     source          1. .102
                     /organism="Escherichia coli"
                     /db_xref="taxon:562"
     rRNA            <1. .>102
                     /product="23S ribosomal RNA"
     modified_base   44
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     conflict        73
                     /citation=[1]
                     /replace=""
BASE COUNT       27 a     22 c     31 g     22 t
ORIGIN
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  Query Match             90.6%;  Score 15.4;  DB 1;  Length 1(2;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db     42 CGGGGTCTTTCCGTCTT 26


RESULT  9
AB041500/c
LOCUS       AB041500                 178 bp    DNA     linear   BCT 18-APR-2000
DEFINITION  Helicobacter pylori gene for 23S rRNA, partial sequence,
            strain:MHP-001.
ACCESSION   AB041500
VERSION     AB041500.1  GI:7576350
KEYWORDS    .
SOURCE      Helicobacter pylori (strain:MHP-001) DNA.
  ORGANISM  Helicobacter pylori
            Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
            Helicobacter.
REFERENCE   1  (bases 1 to 178)
  AUTHORS   Takayama,S. and Suga,M.
  TITLE     Partial nucleotide sequence of the 23S rRNA gene of H.pylori
  JOURNAL   Published Only in DataBase (2000) In press
REFERENCE   2  (bases 1 to 178)
  AUTHORS   Takayama,S. and Suga,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-APR-2000) to the DDBJ/EMBL/GenBank databases.
            Shigenobu Takayama, St Marianna University Yokohamashi Seibu
            Hospital, Division of Laboratory Research; 1197-1 Yazashi Asahiku,
            Yokohama, Kanagawa 241-0811, Japan (E-mail:stakayam@mb.kcom.ne.jp,
            Tel:81-45-366-1111(ex.3352), Fax:81-45-366-1190)
FEATURES             Location/Qualifiers
     source          1. .178
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                     /strain="MHP-001"
                     /db_xref="taxon:210"
                     /note="isolate from a patient who succeeded the
                     eradication therapy by the treatment with AMPC, CAM and
                     PPI."
     rRNA            <1. .>178
                     /product="23S ribosomal RNA"
BASE COUNT       48 a     39 c     49 g     42 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 1;  Length 178;
  Best Local Similarity   94.1%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db     80 CGGGGTCTTTCCGTCTT 64


RESULT  10
GONSP16SR/c
LOCUS       GONSP16SR                372 bp    DNA     linear   VRT 05-JAN-1998
DEFINITION  Gonatodes sp. mitochondrial gene for 16S ribosomal RNA.
ACCESSION   X86060
VERSION     X86060.1  GI:1107569
KEYWORDS    16S ribosomal RNA; 16S rRNA gene.
SOURCE      Gonatodes sp.
  ORGANISM  Mitochondrion Gonatodes sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae;
            Gonatodes.
REFERENCE   1  (bases 1 to 372)
  AUTHORS   Hass,C.A.
  TITLE     Relationships among West Indian geckos of the genus
            Sphaerodactylus: a preliminary analysis of mitochondrial 16S
            ribosomal RNA sequences
  JOURNAL   (in) Powell,R. and Henderson,R.W. (Eds.);
            WEST INDIAN HERPETOLOGY. A TRIBUTE TO ALBERT SCHWARTZ: 1-1;
            Society for the Study of Amphibians and Reptiles (1995)
REFERENCE   2  (bases 1 to 372)
  AUTHORS   Hass,C.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-APR-1995) Hass C.A., The Pennsylvania State
            University, Biology, 208 Mueller, University Park, Pennsylvania,
            USA, 16802
FEATURES             Location/Qualifiers
     source          1. .372
                     /organism="Gonatodes sp."
                     /organelle="mitochondrion"
                     /db_xref="taxon:71166"
                     /tissue_type="tissue homogenate (viscera)"
     rRNA            <1. .>372
                     /gene="16S rRNA"
                     /product="16S ribosomal RNA"
     gene            1. .372
                     /gene="16S rRNA"
BASE COUNT      110 a    109 c     77 g     72 t      4 others
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 372;
  Best Local Similarity   94.1%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    102 CGGGGTCTTCTCGTCTT 86


RESULT  11
AB020407/c
LOCUS       AB020407                 387 bp    DNA     linear   INV 08-APR-2000
DEFINITION  Fasciola sp. (Japanese isolate) mitochondrial DNA for large subunit
            ribosomal RNA.
ACCESSION   AB020407
VERSION     AB020407.1  GI:3978574
KEYWORDS    .
SOURCE      Fasciola sp. (Japanese isolate) (specific_host:Bos taurus) adult
            worm mitochondrion DNA.
  ORGANISM  Fasciola sp. (Japanese isolate)
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Echinostomida; Echinostomata; Fascioloidea; Fasciolidae; Fasciola.
REFERENCE   1  (bases 1 to 387)
  AUTHORS   Nakao,M.
  TITLE     Mitochondrial large subunit rRNA genes in the Platyhelminthes
  JOURNAL   Published Only in DataBase (1998) In press
REFERENCE   2  (bases 1 to 387)
  AUTHORS   Nakao,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-NOV-1998) to the DDBJ/EMBL/GenBank databases. Minoru
            Nakao, Asahikawa Medical College, Department of Parasitology;
            Nishikagura 4-sen 5-go, Asahikawa, Hokkaido 078-8510, Japan
            (E-mail:nakao@asahikawa-med.ac.jp, Tel:81-166-68-2422,
            Fax:81-166-68-2429)
FEATURES             Location/Qualifiers
     source          1. .387
                     /organism="Fasciola sp. (Japanese isolate)"
                     /specific_host="Bos taurus"
                     /db_xref="taxon:85436"
                     /dev_stage="adult worm"
     rRNA            1. .387
                     /product="large subunit ribosomal RNA"
BASE COUNT      101 a     45 c    107 g    134 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 3;  Length 387;
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  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    141 CGGGGTCTTTCCGTCTT 125


RESULT  12
AB020409/c
LOCUS       AB020409                391 bp    DNA     linear   INV 08-APR-2000
DEFINITION  Schistosoma japonicum mitochondrial DNA for large subunit ribosomal
            RNA, partial sequence.
ACCESSION   AB020409
VERSION     AB020409.1  GI:3978576
KEYWORDS    .
SOURCE      Schistosoma japonicum egg mitochondrion DNA.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 391)
  AUTHORS   Nakao,M.
  TITLE     Mitochondrial large subunit rRNA genes in the Platyhelminthes
  JOURNAL   Published Only in DataBase (1998) In press
REFERENCE   2  (bases 1 to 391)
  AUTHORS   Nakao,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-NOV-1998) to the DDBJ/EMBL/GenBank databases. Minoru
            Nakao, Asahikawa Medical College, Department of Parasitology;
            Nishikagura 4-sen 5-go, Asahikawa, Hokkaido 078-8510, Japan
            (E-mail:nakao@asahikawa-med.ac.jp, Tel:81-166-68-2422,
            Fax:81-166-68-2429)
FEATURES             Location/Qualifiers
     source          1. .391
                     /organism="Schistosoma japonicum"
                     /db_xref="taxon:6182"
                     /dev_stage="egg"
     rRNA            <1. .>391
                     /product="large subunit ribosomal RNA"
BASE COUNT      119 a     45 c     84 g    143 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 3;  Length 391;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    139 CGGGGTCTTTCCGTCTT 123


RESULT  13
AF122971/c
LOCUS       AF122971                400 bp    DNA     linear   INV 02-AUG-1999
DEFINITION  Cerastoderma edule 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF122971
VERSION     AF122971.1  GI:5669807
KEYWORDS    .
SOURCE      Cerastoderma edule.
  ORGANISM  Mitochondrion Cerastoderma edule
            Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
            Cardioidea; Cardiidae; Cerastoderma.
REFERENCE   1  (bases 1 to 400)
  AUTHORS   Schneider,J.A. and O'Foighil,D.
  TITLE     Phylogeny of giant clams (Cardiidae: Tridacninae) based on partial
            mitochondrial 16S rDNA gene sequences
  JOURNAL   Mol. Phylogenet. Evol. (1999) In press
REFERENCE   2  (bases 1 to 400)
  AUTHORS   Schneider,J.A. and O'Foighil,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JAN-1999) Geology & Geophysics, University of
            Wisconsin, 1215 W. Dayton St., Madison, WI 53706, USA
FEATURES             Location/Qualifiers
     source          1. .400
                     /organism="Cerastoderma edule"
                     /organelle="mitochondrion"
                     /db_xref="taxon:55710"
     rRNA            <1. .>400
                     /product="16S ribosomal RNA"
BASE COUNT      120 a     68 c     95 g    117 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 3;  Length 400;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          |||||||||| ||||||
Db    202 CGGGGTCTTCTCGTCTT 186


RESULT  14
MTLARNA16/c
LOCUS       MTLARNA16               405 bp    DNA     linear   VRT 23-FEB-1995
DEFINITION  L.albirostris mitochondrial gene for 16S ribosomal RNA.
ACCESSION   Z46487
VERSION     Z46487.1  GI:683622
KEYWORDS    16S ribosomal RNA; 16S rRNA gene.
SOURCE      Liotyphlops albirostris.
  ORGANISM  Mitochondrion Liotyphlops albirostris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Serpentes; Typhlopoidea;
            Anomalepididae; Liotyphlops.
REFERENCE   1  (bases 1 to 405)
  AUTHORS   Heise,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-1994) Heise P. J., Pennsylvania State University,
            Department of Biology, 208 Erwin W. Mueller Laboratory, University
            Park, Pennsylvania, USA, 16802
REFERENCE   2  (bases 1 to 405)
  AUTHORS   Heise,P.J., Maxson,L.R., Dowling,H.G. and Hedges,S.B.
  TITLE     Higher-level snake phylogeny inferred from mitochondrial DNA
            sequences of 12S rRNA and 16S rRNA genes
  JOURNAL   Mol. Biol. Evol. 12 (2), 259-265 (1995)
  MEDLINE   95214537
FEATURES             Location/Qualifiers
     source          1. .405
                     /organism="Liotyphlops albirostris"
                     /organelle="mitochondrion"
                     /db_xref="taxon:39075"
                     /tissue_type="blood"
     rRNA            <1. .>405
                     /gene="16S rRNA gene"
                     /product="16S ribosomal RNA"
     gene            1. .405
                     /gene="16S rRNA gene"
BASE COUNT      128 a    109 c     89 g     77 t      2 others
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 405;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          |||||||||| ||||||
Db    124 CGGGGTCTTCTCGTCTT 108


RESULT  15
AB028789/c
LOCUS       AB028789                420 bp    DNA     linear   VRT 05-AUG-2000
DEFINITION  Mabuya quiquetaeniata mitochondrial gene for 16S rRNA, partial
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            sequence.
ACCESSION   AB028789
VERSION     AB028789.1  GI:8918306
KEYWORDS    16S rRNA; 16S ribosomal RNA.
SOURCE      Mabuya quiquetaeniata mitochondrion DNA.
  ORGANISM  Mitochondrion Mabuya quinquetaeniata
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (sites)
  AUTHORS   Honda,M., Ota,H., Kobayashi,M., Nabhitabhata,J., Yong,H.S. and
            Hikida,T.
  TITLE     Phylogenetic relationships, character evolution, and biogeography
            of the subfamily lygosominae (Reptilia: scincidae) inferred from
            mitochondrial DNA sequences
  JOURNAL   Mol. Phylogenet. Evol. 15 (3), 452-461 (2000)
  MEDLINE   20318524
REFERENCE   2  (bases 1 to 420)
  AUTHORS   Honda,M., Ota,H., Kobayashi,M., Nabhitabhata,J., Yong,H.-S. and
            Hikida,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JUN-1999) to the DDBJ/EMBL/GenBank databases.
            Hidetoshi Ota, University of the Ryukyu, Bisphere Research Center;
            1, Senbaru, Nishihar-cho, Okinawa 903-0213, Japan
            (Tel:+81-98-895-8937, Fax:+81-98-895-8576)
FEATURES             Location/Qualifiers
     source          1. .420
                     /organism="Mabuya quinquetaeniata"
                     /organelle="mitochondrion"
                     /db_xref="taxon:96430"
     rRNA            <1. .>420
                     /product="16S rRNA"
BASE COUNT      136 a    110 c     86 g     88 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 420;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    124 CGGGGTCTTCTCGTCTT 108


RESULT  16
AB028791/c
LOCUS       AB028791                 421 bp    DNA     linear   VRT 05-AUG-2000
DEFINITION  Mabuya striata mitochondrial gene for 16S rRNA, partial sequence.
ACCESSION   AB028791
VERSION     AB028791.1  GI:8918308
KEYWORDS    16S rRNA; 16S ribosomal RNA.
SOURCE      Mabuya striata mitochondrion DNA.
  ORGANISM  Mitochondrion Mabuya striata
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (sites)
  AUTHORS   Honda,M., Ota,H., Kobayashi,M., Nabhitabhata,J., Yong,H.S. and
            Hikida,T.
  TITLE     Phylogenetic relationships, character evolution, and biogeography
            of the subfamily lygosominae (Reptilia: scincidae) inferred from
            mitochondrial DNA sequences
  JOURNAL   Mol. Phylogenet. Evol. 15 (3), 452-461 (2000)
  MEDLINE   20318524
REFERENCE   2  (bases 1 to 421)
  AUTHORS   Honda,M., Ota,H., Kobayashi,M., Nabhitabhata,J., Yong,H.-S. and
            Hikida,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JUN-1999) to the DDBJ/EMBL/GenBank databases.
            Hidetoshi Ota, University of the Ryukyu, Bisphere Research Center;
            1, Senbaru, Nishihar-cho, Okinawa 903-0213, Japan
            (Tel:+81-98-895-8937, Fax:+81-98-895-8576)
FEATURES             Location/Qualifiers
     source          1. .421
                     /organism="Mabuya striata"
                     /organelle="mitochondrion"
                     /db_xref="taxon:96723"
     rRNA            <1. .>421
                     /product="16S rRNA"
BASE COUNT      144 a     96 c     82 g     99 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 421;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    124 CGGGGTCTTCTCGTCTT 108


RESULT  17
MTALIM16S/c
LOCUS       MTALIM16S                427 bp    DNA     linear   VRT 30-AUG-1995
DEFINITION  A.limifrons mitochondrial gene for 16S ribosomal RNA.
ACCESSION   Z48657
VERSION     Z48657.1  GI:732838
KEYWORDS    16S ribosomal RNA; 16S rRNA gene.
SOURCE      Anolis limifrons.
  ORGANISM  Anolis limifrons
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
REFERENCE   1  (bases 1 to 427)
  AUTHORS   Hass,C.A., Hedges,S.B. and Maxson,L.R.
  TITLE     Molecular insights into the relationships and biogeography of West
            Indian anoline lizards
  JOURNAL   Biochem. Syst. Ecol. 21, 97-114 (1993)
REFERENCE   2  (bases 1 to 427)
  AUTHORS   Hass,C.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAR-1995) Hass C. A., The Pennsylvania State
            University, Biology, 208 Mueller, University Park, Pennsylvania,
            USA, 16802
FEATURES             Location/Qualifiers
     source          1. .427
                     /organism="Anolis limifrons"
                     /db_xref="taxon:38897"
                     /tissue_type="liver"
     rRNA            <1. .>427
                     /gene="16S rRNA"
                     /product="16S ribosomal RNA"
     gene            1. .427
                     /gene="16S rRNA"
BASE COUNT      149 a     84 c     77 g    117 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 427;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    124 CGGGGTCTTCTCGTCTT 108


RESULT  18
LCU39982/c
LOCUS       LCU39982                 436 bp    DNA     linear   VRT 03-AUG-1996
DEFINITION  Litoria cyclorhynchus 16S ribosomal RNA gene, mitochondrial gene
            encoding mitochondrial rRNA, partial sequence.
ACCESSION   U39982
VERSION     U39982.1  GI:1465720
KEYWORDS    .
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```
SOURCE      Litoria cyclorhynchus.
  ORGANISM  Mitochondrion Litoria cyclorhynchus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
            Litoria.
REFERENCE   1  (bases 1 to 436)
  AUTHORS   Ruvinsky,I. and Maxson,L.R.
  TITLE     Phylogenetic relationships among bufonoid frogs
            (Anura:Neobatrachia) inferred from mitochondrial DNA sequences
  JOURNAL   Mol. Phylogenet. Evol. 5 (3), 533-547 (1996)
  MEDLINE   96364023
REFERENCE   2  (bases 1 to 436)
  AUTHORS   Ruvinsky,I. and Maxson,L.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-NOV-1995) Ilya Ruvinsky Molecular Biology, Princeton
            University, Lewis Thomas Laboratory, Princeton, NJ 08544, USA
FEATURES             Location/Qualifiers
     source          1. .436
                     /organism="Litoria cyclorhynchus"
                     /organelle="mitochondrion"
                     /db_xref="taxon:44373"
                     /note="Fragment=16S1"
     rRNA            <1. .>436
                     /product="16S ribosomal RNA"
BASE COUNT      128 a    118 c     92 g     98 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 436;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    124 CGGGGTCTTCTCGTCTT 108


RESULT 19
AF122972/c
LOCUS       AF122972                439 bp    DNA     linear   INV 02-AUG-1999
DEFINITION  Cerastoderma glaucum 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF122972
VERSION     AF122972.1  GI:5669808
KEYWORDS    .
SOURCE      Cerastoderma glaucum.
  ORGANISM  Mitochondrion Cerastoderma glaucum
            Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
            Cardioidea; Cardiidae; Cerastoderma.
REFERENCE   1  (bases 1 to 439)
  AUTHORS   Schneider,J.A. and O'Foighil,D.
  TITLE     Phylogeny of giant clams (Cardiidae: Tridacninae) based on partial
            mitochondrial 16S rDNA gene sequences
  JOURNAL   Mol. Phylogenet. Evol. (1999) In press
REFERENCE   2  (bases 1 to 439)
  AUTHORS   Schneider,J.A. and O'Foighil,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JAN-1999) Geology & Geophysics, University of
            Wisconsin, 1215 W. Dayton St., Madison, WI 53706, USA
FEATURES             Location/Qualifiers
     source          1. .439
                     /organism="Cerastoderma glaucum"
                     /organelle="mitochondrion"
                     /db_xref="taxon:94722"
     rRNA            <1. .>439
                     /product="16S ribosomal RNA"
BASE COUNT      127 a     80 c    108 g    124 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 3;  Length 439;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    202 CGGGGTCTTCTCGTCTT 186


RESULT 20
AF152022/c
LOCUS       AF152022                441 bp    DNA     linear   INV 13-JUN-2000
DEFINITION  Corbicula africana 16S large subunit ribosomal RNA gene, partial
            sequence; mitochondrial gene for mitochondrial product.
ACCESSION   AF152022
VERSION     AF152022.1  GI:8489065
KEYWORDS    .
SOURCE      Corbicula madagascariensis.
  ORGANISM  Mitochondrion Corbicula madagascariensis
            Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
            Corbiculoidea; Corbiculidae; Corbicula.
REFERENCE   1  (bases 1 to 441)
  AUTHORS   Cooley,L.R. and O'Foighil,D.
  TITLE     Phylogenetic analysis of the Sphaeriidae (Mollusca: Bivalvia) based
            on partial mitochondrial 16S rDNA gene sequences
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 441)
  AUTHORS   Cooley,L.R. and O'Foighil,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-MAY-1999) Museum of Zoology, University of Michigan,
            1109 Geddes Ave, Ann Arbor, MI 48109-1079, USA
FEATURES             Location/Qualifiers
     source          1. .441
                     /organism="Corbicula madagascariensis"
                     /organelle="mitochondrion"
                     /db_xref="taxon:127827"
                     /country="Madagascar"
                     /note="collected in 1996"
     rRNA            <1. .>441
                     /product="16S large subunit ribosomal RNA"
BASE COUNT      151 a     54 c     95 g    141 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 3;  Length 441;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    197 CGGGGTCTTCTCGTCTT 181


RESULT 21
AF152024/c
LOCUS       AF152024                442 bp    DNA     linear   INV 13-JUN-2000
DEFINITION  Corbicula fluminea 16S large subunit ribosomal RNA gene, partial
            sequence; mitochondrial gene for mitochondrial product.
ACCESSION   AF152024
VERSION     AF152024.1  GI:8489067
KEYWORDS    .
SOURCE      Corbicula fluminea.
  ORGANISM  Mitochondrion Corbicula fluminea
            Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
            Corbiculoidea; Corbiculidae; Corbicula.
REFERENCE   1  (bases 1 to 442)
  AUTHORS   Cooley,L.R. and O'Foighil,D.
  TITLE     Phylogenetic analysis of the Sphaeriidae (Mollusca: Bivalvia) based
            on partial mitochondrial 16S rDNA gene sequences
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 442)
  AUTHORS   Cooley,L.R. and O'Foighil,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-MAY-1999) Museum of Zoology, University of Michigan,
            1109 Geddes Ave, Ann Arbor, MI 48109-1079, USA
FEATURES             Location/Qualifiers
```

```
     source          1. .442
                     /organism="Corbicula fluminea"
                     /organelle="mitochondrion"
                     /db_xref="taxon:45949"
                     /country="USA: Michigan, Huron River, Ann Arbor"
                     /note="collected in 1996"
     rRNA            <1. .>442
                     /product="16S large subunit ribosomal RNA"
BASE COUNT      150 a     53 c     99 g    140 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 3;  Length 442;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          |||||||||| ||||||
Db    197 CGGGGTCTTCTCGTCTT 181


RESULT  22
AF152023/c
LOCUS       AF152023               443 bp    DNA     linear   INV 13-JUN-2000
DEFINITION  Corbicula australis 16S large subunit ribosomal RNA gene, partial
            sequence; mitochondrial gene for mitochondrial product.
ACCESSION   AF152023
VERSION     AF152023.1  GI:8489066
KEYWORDS    .
SOURCE      Corbicula australis.
  ORGANISM  Mitochondrion Corbicula australis
            Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
            Corbiculoidea; Corbiculidae; Corbicula.
REFERENCE   1  (bases 1 to 443)
  AUTHORS   Cooley,L.R. and O'Foighil,D.
  TITLE     Phylogenetic analysis of the Sphaeriidae (Mollusca: Bivalvia) based
            on partial mitochondrial 16S rDNA gene sequences
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 443)
  AUTHORS   Cooley,L.R. and O'Foighil,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-MAY-1999) Museum of Zoology, University of Michigan,
            1109 Geddes Ave, Ann Arbor, MI 48109-1079, USA
FEATURES             Location/Qualifiers
     source          1. .443
                     /organism="Corbicula australis"
                     /organelle="mitochondrion"
                     /db_xref="taxon:127828"
                     /country="Australia: New South Wales"
                     /note="collected in 1996"
     rRNA            <1. .>443
                     /product="16S large subunit ribosomal RNA"
BASE COUNT      150 a     54 c     99 g    140 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 3;  Length 443;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          |||||||||| ||||||
Db    197 CGGGGTCTTCTCGTCTT 181


RESULT  23
SEOMTRGAJ/c
LOCUS       SEOMTRGAJ              451 bp    DNA     linear   VRT 11-JAN-1996
DEFINITION  Sceloporus variabilis mitochondrial 16S ribosomal RNA (16S rRNA)
            gene, partial.
ACCESSION   L41479
VERSION     L41479.1  GI:1050357
KEYWORDS    16S ribosomal RNA; ribosomal RNA.
SOURCE      Mitochondrion Sceloporus variabilis DNA.
  ORGANISM  Mitochondrion Sceloporus variabilis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
            Sceloporus.
REFERENCE   1  (bases 1 to 451)
  AUTHORS   Reeder,T.W.
  TITLE     Phylogenetic relationships among phrynosomatid lizards as inferred
            from mitochondrial ribosomal DNA sequences: substitutional bias and
            information content of transitions relative to transversions
  JOURNAL   Mol. Phylogenet. Evol. 4 (2), 203-222 (1995)
  MEDLINE   95392830
FEATURES             Location/Qualifiers
     source          1. .451
                     /organism="Sceloporus variabilis"
                     /organelle="mitochondrion"
                     /db_xref="taxon:43638"
     rRNA            <1. .>451
                     /gene="16S rRNA"
                     /product="16S ribosomal RNA"
     gene            1. .451
                     /gene="16S rRNA"
BASE COUNT      150 a    106 c     89 g    102 t      4 others
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 451;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          |||||||||| ||||||
Db    169 CGGGGTCTTCTCGTCTT 153


RESULT  24
SCAF000830/c
LOCUS       SCAF000830             455 bp    DNA     linear   VRT 03-SEP-1997
DEFINITION  Sceloporus cozumelae 16S ribosomal RNA gene, mitochondrial gene for
            mitochondrial RNA,partial sequence.
ACCESSION   AF000830
VERSION     AF000830.1  GI:2352190
KEYWORDS    .
SOURCE      Sceloporus cozumelae.
  ORGANISM  Mitochondrion Sceloporus cozumelae
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
            Sceloporus.
REFERENCE   1  (bases 1 to 455)
  AUTHORS   Wiens,J.J. and Reeder,T.W.
  TITLE     Phylogeny of the spiny lizards (Sceloporus) based on molecular and
            morphological evidence
  JOURNAL   Herpetological Monographs 11 (1997) In press
REFERENCE   2  (bases 1 to 455)
  AUTHORS   Wiens,J.J. and Reeder,T.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-APR-1997) Biology, San Diego State University, San
            Diego, CA 92182-4614, USA
FEATURES             Location/Qualifiers
     source          1. .455
                     /organism="Sceloporus cozumelae"
                     /organelle="mitochondrion"
                     /db_xref="taxon:59696"
     rRNA            <1. .>455
                     /product="16S ribosomal RNA"
BASE COUNT      149 a    106 c     93 g    104 t      3 others
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 455;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    170 CGGGGTCTTCTCGTCTT 154


RESULT  25
AF038999/c
LOCUS       AF038999                457 bp    DNA     linear   INV 11-MAR-1999
DEFINITION  Corbicula fluminea 16S ribosomal RNA gene, mitochondrial gene for
            mitochondrial RNA, partial sequence.
ACCESSION   AF038999
VERSION     AF038999.1  GI:4104737
KEYWORDS    .
SOURCE      Corbicula fluminea.
  ORGANISM  Mitochondrion Corbicula fluminea
            Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
            Corbiculoidea; Corbiculidae; Corbicula.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Stepien,C.A., Hubers,A.N. and Skidmore,J.L.
  TITLE     Diagnostic genetic markers and evolutionary relationships among
            dreissenoid and corbiculoid bivalves: Phylogenetic signal from
            mitochondrial 16S rDNA
  JOURNAL   Mol. Phylogenet. Evol. 10 (1999) In press
REFERENCE   2  (bases 1 to 457)
  AUTHORS   Stepien,C.A. and Hubers,A.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-DEC-1997) Biology, Case Western Reserve University,
            10900 Euclid Ave., Cleveland, OH 44106, USA
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Corbicula fluminea"
                     /organelle="mitochondrion"
                     /db_xref="taxon:45949"
     rRNA            <1. .>457
                     /product="16S ribosomal RNA"
BASE COUNT      158 a     53 c     97 g    149 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 3;  Length 457;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    205 CGGGGTCTTCTCGTCTT 189


RESULT  26
SSAF000868/c
LOCUS       SSAF000868              457 bp    DNA     linear   VRT 03-SEP-1997
DEFINITION  Sceloporus smithi 16S ribosomal RNA gene, mitochondrial gene for
            mitochondrial RNA,partial sequence.
ACCESSION   AF000868
VERSION     AF000868.1  GI:2352228
KEYWORDS    .
SOURCE      Sceloporus smithi.
  ORGANISM  Mitochondrion Sceloporus smithi
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
            Sceloporus.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Wiens,J.J. and Reeder,T.W.
  TITLE     Phylogeny of the spiny lizards (Sceloporus) based on molecular and
            morphological evidence
  JOURNAL   Herpetological Monographs 11 (1997) In press
REFERENCE   2  (bases 1 to 457)
  AUTHORS   Wiens,J.J. and Reeder,T.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-APR-1997) Biology, San Diego State University, San
            Diego, CA 92182-4614, USA
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Sceloporus smithi"
                     /organelle="mitochondrion"
                     /db_xref="taxon:59721"
     rRNA            <1. .>457
                     /product="16S ribosomal RNA"
BASE COUNT      153 a    109 c     89 g    106 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 457;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    170 CGGGGTCTTCTCGTCTT 154


RESULT  27
CGL243574/c
LOCUS       CGL243574               459 bp    DNA     linear   INV 03-FEB-2000
DEFINITION  Chlamys glabra partial mitochondrial 16S rRNA gene.
ACCESSION   AJ243574
VERSION     AJ243574.1  GI:6624899
KEYWORDS    16S ribosomal RNA; 16S rRNA gene.
SOURCE      Chlamys glabra.
  ORGANISM  Mitochondrion Chlamys glabra
            Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pectinoida;
            Pectinoidea; Pectinidae; Chlamys.
REFERENCE   1  (bases 1 to 459)
  AUTHORS   Canapa,A., Barucca,M., Marinelli,A. and Olmo,E.
  TITLE     Molecular data from the 16S rRNA gene for the phylogeny of
            Pectinidae
  JOURNAL   J. Mol. Evol. 50 (1), 93-97 (2000)
  MEDLINE   20119759
REFERENCE   2  (bases 1 to 459)
  AUTHORS   Canapa,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-JUL-1999) Canapa A., Istituto di Biologia e Genetica,
            Ancona University, Via Brecce Bianche, I-60131, ITALY
FEATURES             Location/Qualifiers
     source          1. .459
                     /organism="Chlamys glabra"
                     /organelle="mitochondrion"
                     /db_xref="taxon:100772"
     rRNA            <1. .>459
                     /gene="16S rRNA"
                     /product="16S ribosomal RNA"
     gene            1. .459
                     /gene="16S rRNA"
BASE COUNT      117 a     76 c    120 g    146 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 3;  Length 459;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    207 CGGGGTCTTCTCGTCTT 191


RESULT  28
AF113638/c
LOCUS       AF113638                459 bp    DNA     linear   VRT 17-JUN-1999
DEFINITION  Hydromedusa tectifera 16S ribosomal RNA gene, mitochondrial gene
            for mitochondrial RNA, partial sequence.
ACCESSION   AF113638
VERSION     AF113638.1  GI:4633172
KEYWORDS    .
SOURCE      Hydromedusa tectifera.
  ORGANISM  Mitochondrion Hydromedusa tectifera
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           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Testudines; Pleurodira; Chelidae; Hydromedusa.
REFERENCE  1  (bases 1 to 459)
  AUTHORS  Georges,A., Birrell,J., Saint,K.M., McCord,W. and Donnellan,S.C.
  TITLE    A phylogeny for side-necked turtles (Chelonia: Pleurodira) based on
           mitochondrial and nuclear sequence variation
  JOURNAL  Unpublished
REFERENCE  2  (bases 1 to 459)
  AUTHORS  Georges,A., Birrell,J., Saint,K.M., McCord,W. and Donnellan,S.C.
  TITLE    Direct Submission
  JOURNAL  Submitted (16-DEC-1998) Applied Ecology Research Group and CRC for
           Freshwater Ecology, University of Canberra, Canberra, ACT 2601,
           Australia
FEATURES             Location/Qualifiers
     source          1. .459
                     /organism="Hydromedusa tectifera"
                     /organelle="mitochondrion"
                     /db_xref="taxon:61327"
     rRNA            <1. .>459
                     /product="16S ribosomal RNA"
BASE COUNT      150 a     98 c     85 g    109 t     17 others
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 459;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    175 CGGGGTCTTCTCGTCTT 159


RESULT  29
AF360118/c
LOCUS       AF360118                482 bp    DNA     linear   INV 24-APR-2001
DEFINITION  Carybdea marsupialis 16S ribosomal RNA gene, partial sequence;
           mitochondrial gene for mitochondrial product.
ACCESSION   AF360118
VERSION     AF360118.1  GI:13774986
KEYWORDS    .
SOURCE      Carybdea marsupialis.
  ORGANISM  Mitochondrion Carybdea marsupialis
           Eukaryota; Metazoa; Cnidaria; Cubozoa; Cubomedusae; Carybdeidae;
           Carybdea.
REFERENCE  1  (bases 1 to 482)
  AUTHORS  Ender,A. and Schierwater,B.
  TITLE    The limitation of 16S rDNA data for resolving phylogenetic
           relationships in diploblastic animals
  JOURNAL  Unpublished
REFERENCE  2  (bases 1 to 482)
  AUTHORS  Ender,A. and Schierwater,B.
  TITLE    Direct Submission
  JOURNAL  Submitted (13-MAR-2001) Ecology and Evolution, Institut fuer
           Tieroekologie und Zellbiologie, Buenteweg 17d, Hannover D-30559,
           Germany
FEATURES             Location/Qualifiers
     source          1. .482
                     /organism="Carybdea marsupialis"
                     /organelle="mitochondrion"
                     /db_xref="taxon:157781"
     rRNA            <1. .>482
                     /product="16S ribosomal RNA"
BASE COUNT      155 a     94 c    116 g    117 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 3;  Length 482;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    217 CGGGGTCTTCTCGTCTT 201


RESULT  30
ACO243882/c
LOCUS       ACO243882               487 bp    DNA     linear   INV 03-FEB-2000
DEFINITION  Adamussium colbecki partial mitochondrial 16S rRNA gene.
ACCESSION   AJ243882
VERSION     AJ243882.1  GI:6624883
KEYWORDS    16S ribosomal RNA; 16S rRNA gene.
SOURCE      Adamussium colbecki.
  ORGANISM  Mitochondrion Adamussium colbecki
           Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pectinoida;
           Pectinoidea; Pectinidae; Adamussium.
REFERENCE  1  (bases 1 to 487)
  AUTHORS  Canapa,A., Barucca,M., Marinelli,A. and Olmo,E.
  TITLE    Molecular data from the 16S rRNA gene for the phylogeny of
           Pectinidae
  JOURNAL  J. Mol. Evol. 50 (1), 93-97 (2000)
  MEDLINE  20119759
REFERENCE  2  (bases 1 to 487)
  AUTHORS  Canapa,A.
  TITLE    Direct Submission
  JOURNAL  Submitted (26-JUL-1999) Canapa A., Istituto di Biologia e Genetica,
           Ancona University, Via Brecce Bianche, I-60131, ITALY
FEATURES             Location/Qualifiers
     source          1. .487
                     /organism="Adamussium colbecki"
                     /organelle="mitochondrion"
                     /db_xref="taxon:95546"
     rRNA            <1. .>487
                     /gene="16S rRNA"
                     /product="16S ribosomal RNA"
     gene            1. .487
                     /gene="16S rRNA"
BASE COUNT      110 a     91 c    147 g    139 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 3;  Length 487;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    209 CGGGGTCTTCTCGTCTT 193


RESULT  31
AF153560/c
LOCUS       AF153560                490 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya acutilabris 16S ribosomal RNA gene, partial sequence;
           mitochondrial gene for mitochondrial product.
ACCESSION   AF153560
VERSION     AF153560.1  GI:8885799
KEYWORDS    .
SOURCE      Mabuya acutilabris.
  ORGANISM  Mitochondrion Mabuya acutilabris
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
           Scincidae; Mabuya.
REFERENCE  1  (bases 1 to 490)
  AUTHORS  Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE    First Data on the Molecular Phylogeography of Scincid Lizards of
           the Genus Mabuya
  JOURNAL  Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
  PUBMED   11020300
REFERENCE  2  (bases 1 to 490)
  AUTHORS  Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE    Direct Submission
  JOURNAL  Submitted (24-MAY-1999) Herpetology, Zoologisches
           Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, Bonn,
           NRW 53113, Germany
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FEATURES             Location/Qualifiers
     source          1. .490
                     /organism="Mabuya acutilabris"
                     /organelle="mitochondrion"
                     /db_xref="taxon:111163"
     rRNA            <1. .>490
                     /product="16S ribosomal RNA"
BASE COUNT      162 a    127 c    102 g     99 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 490;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtctt 17
           ||||||||||| ||||||
Db     197 CGGGGTCTTCTCGTCTT 181


RESULT  32
AF153562/c
LOCUS       AF153562                 490 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya binotata 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF153562
VERSION     AF153562.1  GI:8885801
KEYWORDS    .
SOURCE      Mabuya binotata.
  ORGANISM  Mitochondrion Mabuya binotata
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (bases 1 to 490)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     First Data on the Molecular Phylogeography of Scincid Lizards of
            the Genus Mabuya
  JOURNAL   Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
   PUBMED   11020300
REFERENCE   2  (bases 1 to 490)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1999) Herpetology, Zoologisches
            Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, Bonn,
            NRW 53113, Germany
FEATURES             Location/Qualifiers
     source          1. .490
                     /organism="Mabuya binotata"
                     /organelle="mitochondrion"
                     /db_xref="taxon:111165"
     rRNA            <1. .>490
                     /product="16S ribosomal RNA"
BASE COUNT      165 a    125 c     99 g    101 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 490;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtctt 17
           ||||||||||| ||||||
Db     197 CGGGGTCTTCTCGTCTT 181


RESULT  33
AF153569/c
LOCUS       AF153569                 504 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya hoeschi 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF153569
VERSION     AF153569.1  GI:8885808
KEYWORDS    .
SOURCE      Mabuya hoeschi.
  ORGANISM  Mitochondrion Mabuya hoeschi
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (bases 1 to 504)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     First Data on the Molecular Phylogeography of Scincid Lizards of
            the Genus Mabuya
  JOURNAL   Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
   PUBMED   11020300
REFERENCE   2  (bases 1 to 504)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1999) Herpetology, Zoologisches
            Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, Bonn,
            NRW 53113, Germany
FEATURES             Location/Qualifiers
     source          1. .504
                     /organism="Mabuya hoeschi"
                     /organelle="mitochondrion"
                     /db_xref="taxon:111178"
     rRNA            <1. .>504
                     /product="16S ribosomal RNA"
BASE COUNT      161 a    125 c    104 g    114 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 504;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtctt 17
           ||||||||||| ||||||
Db     195 CGGGGTCTTCTCGTCTT 179


RESULT  34
AF153571/c
LOCUS       AF153571                 504 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya irregularis 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF153571
VERSION     AF153571.1  GI:8885810
KEYWORDS    .
SOURCE      Mabuya irregularis.
  ORGANISM  Mitochondrion Mabuya irregularis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (bases 1 to 504)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     First Data on the Molecular Phylogeography of Scincid Lizards of
            the Genus Mabuya
  JOURNAL   Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
   PUBMED   11020300
REFERENCE   2  (bases 1 to 504)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1999) Herpetology, Zoologisches
            Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, Bonn,
            NRW 53113, Germany
FEATURES             Location/Qualifiers
     source          1. .504
                     /organism="Mabuya irregularis"
                     /organelle="mitochondrion"
                     /db_xref="taxon:111180"
     rRNA            <1. .>504
                     /product="16S ribosomal RNA"
BASE COUNT      165 a    121 c    100 g    117 t      1 others
ORIGIN
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  Query Match             90.6%;  Score 15.4;  DB 5;  Length 504;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    198 CGGGGTCTTCTCGTCTT 182


RESULT  35
AF153575/c
LOCUS       AF153575                 504 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya margeritifera 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF153575
VERSION     AF153575.1  GI:8885814
KEYWORDS    .
SOURCE      Mabuya margaritifera.
  ORGANISM  Mitochondrion Mabuya margaritifera
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (bases 1 to 504)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     First Data on the Molecular Phylogeography of Scincid Lizards of
            the Genus Mabuya
  JOURNAL   Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
   PUBMED   11020300
REFERENCE   2  (bases 1 to 504)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1999) Herpetology, Zoologisches
            Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, Bonn,
            NRW 53113, Germany
FEATURES             Location/Qualifiers
     source          1. .504
                     /organism="Mabuya margaritifera"
                     /organelle="mitochondrion"
                     /db_xref="taxon:96435"
     rRNA            <1. .>504
                     /product="16S ribosomal RNA"
BASE COUNT      159 a    138 c    102 g    105 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 504;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    197 CGGGGTCTTCTCGTCTT 181


RESULT  36
AF153579/c
LOCUS       AF153579                 504 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya quinquetaeniata 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF153579
VERSION     AF153579.1  GI:8885818
KEYWORDS    .
SOURCE      Mabuya quinquetaeniata.
  ORGANISM  Mitochondrion Mabuya quinquetaeniata
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (bases 1 to 504)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     First Data on the Molecular Phylogeography of Scincid Lizards of
            the Genus Mabuya
  JOURNAL   Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
   PUBMED   11020300
REFERENCE   2  (bases 1 to 504)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1999) Herpetology, Zoologisches
            Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, Bonn,
            NRW 53113, Germany
FEATURES             Location/Qualifiers
     source          1. .504
                     /organism="Mabuya quinquetaeniata"
                     /organelle="mitochondrion"
                     /db_xref="taxon:96430"
     rRNA            <1. .>504
                     /product="16S ribosomal RNA"
BASE COUNT      156 a    131 c    107 g    110 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 504;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    196 CGGGGTCTTCTCGTCTT 180


RESULT  37
AF153584/c
LOCUS       AF153584                 504 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya varia 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF153584
VERSION     AF153584.1  GI:8885823
KEYWORDS    .
SOURCE      Mabuya varia.
  ORGANISM  Mitochondrion Mabuya varia
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (bases 1 to 504)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     First Data on the Molecular Phylogeography of Scincid Lizards of
            the Genus Mabuya
  JOURNAL   Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
   PUBMED   11020300
REFERENCE   2  (bases 1 to 504)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1999) Herpetology, Zoologisches
            Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, Bonn,
            NRW 53113, Germany
FEATURES             Location/Qualifiers
     source          1. .504
                     /organism="Mabuya varia"
                     /organelle="mitochondrion"
                     /db_xref="taxon:111192"
     rRNA            <1. .>504
                     /product="16S ribosomal RNA"
BASE COUNT      165 a    128 c     99 g    112 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 504;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    198 CGGGGTCTTCTCGTCTT 182


RESULT  38
AF153564/c
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LOCUS       AF153564                505 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya capensis 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF153564
VERSION     AF153564.1  GI:8885803
KEYWORDS    .
SOURCE      Mabuya capensis.
  ORGANISM  Mitochondrion Mabuya capensis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (bases 1 to 505)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     First Data on the Molecular Phylogeography of Scincid Lizards of
            the Genus Mabuya
  JOURNAL   Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
   PUBMED   11020300
REFERENCE   2  (bases 1 to 505)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1999) Herpetology, Zoologisches
            Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, Bonn,
            NRW 53113, Germany
FEATURES             Location/Qualifiers
     source          1. .505
                     /organism="Mabuya capensis"
                     /organelle="mitochondrion"
                     /db_xref="taxon:111172"
     rRNA            <1. .>505
                     /product="16S ribosomal RNA"
BASE COUNT      155 a    131 c    103 g    116 t
ORIGIN
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  Query Match             90.6%;  Score 15.4;  DB 5;  Length 505;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    195 CGGGGTCTTCTCGTCTT 179
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RESULT  39
AF153578/c
LOCUS       AF153578                505 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya perroteti 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF153578
VERSION     AF153578.1  GI:8885817
KEYWORDS    .
SOURCE      Mabuya perrotetii.
  ORGANISM  Mitochondrion Mabuya perrotetii
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (bases 1 to 505)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     First Data on the Molecular Phylogeography of Scincid Lizards of
            the Genus Mabuya
  JOURNAL   Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
   PUBMED   11020300
REFERENCE   2  (bases 1 to 505)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1999) Herpetology, Zoologisches
            Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, Bonn,
            NRW 53113, Germany
FEATURES             Location/Qualifiers
     source          1. .505
                     /organism="Mabuya perrotetii"
                     /organelle="mitochondrion"
                     /db_xref="taxon:111182"
     rRNA            <1. .>505
                     /product="16S ribosomal RNA"
BASE COUNT      168 a    131 c     99 g    107 t
ORIGIN
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  Query Match             90.6%;  Score 15.4;  DB 5;  Length 505;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    196 CGGGGTCTTCTCGTCTT 180
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RESULT  40
AF153580/c
LOCUS       AF153580                505 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya spilogaster 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF153580
VERSION     AF153580.1  GI:8885819
KEYWORDS    .
SOURCE      Mabuya spilogaster.
  ORGANISM  Mitochondrion Mabuya spilogaster
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (bases 1 to 505)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     First Data on the Molecular Phylogeography of Scincid Lizards of
            the Genus Mabuya
  JOURNAL   Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
   PUBMED   11020300
REFERENCE   2  (bases 1 to 505)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1999) Herpetology, Zoologisches
            Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, Bonn,
            NRW 53113, Germany
FEATURES             Location/Qualifiers
     source          1. .505
                     /organism="Mabuya spilogaster"
                     /organelle="mitochondrion"
                     /db_xref="taxon:111183"
     rRNA            <1. .>505
                     /product="16S ribosomal RNA"
BASE COUNT      168 a    123 c     99 g    115 t
ORIGIN
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  Query Match             90.6%;  Score 15.4;  DB 5;  Length 505;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    197 CGGGGTCTTCTCGTCTT 181
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RESULT  41
AF153565/c
LOCUS       AF153565                506 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya comorensis 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF153565
VERSION     AF153565.1  GI:8885804
KEYWORDS    .
SOURCE      Mabuya comorensis.
  ORGANISM  Mitochondrion Mabuya comorensis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
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REFERENCE   1  (bases 1 to 506)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     First Data on the Molecular Phylogeography of Scincid Lizards of
            the Genus Mabuya
  JOURNAL   Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
   PUBMED   11020300
REFERENCE   2  (bases 1 to 506)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1999) Herpetology, Zoologisches
            Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, Bonn,
            NRW 53113, Germany
FEATURES             Location/Qualifiers
     source          1. .506
                     /organism="Mabuya comorensis"
                     /organelle="mitochondrion"
                     /db_xref="taxon:111175"
     rRNA            <1. .>506
                     /product="16S ribosomal RNA"
BASE COUNT      165 a    130 c    102 g    108 t      1 others
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 506;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtctt 17
           ||||||||||| ||||||
Db     194 CGGGGTCTTCTCGTCTT 178


RESULT  42
AF153574/c
LOCUS       AF153574                 506 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya maculilabris 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF153574
VERSION     AF153574.1  GI:8885813
KEYWORDS    .
SOURCE      Mabuya maculilabris.
  ORGANISM  Mitochondrion Mabuya maculilabris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (bases 1 to 506)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     First Data on the Molecular Phylogeography of Scincid Lizards of
            the Genus Mabuya
  JOURNAL   Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
   PUBMED   11020300
REFERENCE   2  (bases 1 to 506)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1999) Herpetology, Zoologisches
            Forschungsinstitut und Museum A. Koenig, Adenaueral.ee 160, Bonn,
            NRW 53113, Germany
FEATURES             Location/Qualifiers
     source          1. .506
                     /organism="Mabuya maculilabris"
                     /organelle="mitochondrion"
                     /db_xref="taxon:111194"
     rRNA            <1. .>506
                     /product="16S ribosomal RNA"
BASE COUNT      162 a    134 c    104 g    106 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 506;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtctt 17
           ||||||||||| ||||||
Db     194 CGGGGTCTTCTCGTCTT 178


RESULT  43
AF153577/c
LOCUS       AF153577                 506 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya occidentalis 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF153577
VERSION     AF153577.1  GI:8885816
KEYWORDS    .
SOURCE      Mabuya occidentalis.
  ORGANISM  Mitochondrion Mabuya occidentalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (bases 1 to 506)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     First Data on the Molecular Phylogeography of Scincid Lizards of
            the Genus Mabuya
  JOURNAL   Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
   PUBMED   11020300
REFERENCE   2  (bases 1 to 506)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1999) Herpetology, Zoologisches
            Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, Bonn,
            NRW 53113, Germany
FEATURES             Location/Qualifiers
     source          1. .506
                     /organism="Mabuya occidentalis"
                     /organelle="mitochondrion"
                     /db_xref="taxon:111181"
     rRNA            <1. .>506
                     /product="16S ribosomal RNA"
BASE COUNT      156 a    129 c    104 g    117 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 506;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtctt 17
           ||||||||||| ||||||
Db     196 CGGGGTCTTCTCGTCTT 180


RESULT  44
AF153570/c
LOCUS       AF153570                 507 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya homalocephala 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF153570
VERSION     AF153570.1  GI:8885809
KEYWORDS    .
SOURCE      Mabuya homalocephala.
  ORGANISM  Mitochondrion Mabuya homalocephala
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (bases 1 to 507)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     First Data on the Molecular Phylogeography of Scincid Lizards of
            the Genus Mabuya
  JOURNAL   Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
   PUBMED   11020300
REFERENCE   2  (bases 1 to 507)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1999) Herpetology, Zoologisches
            Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, Bonn,
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           NRW 53113, Germany
FEATURES             Location/Qualifiers
     source          1. .507
                     /organism="Mabuya homalocephala"
                     /organelle="mitochondrion"
                     /db_xref="taxon:111179"
     rRNA            <1. .>507
                     /product="16S ribosomal RNA"
BASE COUNT      164 a    129 c    105 g    108 t      1 others
ORIGIN


  Query Match           90.6%;  Score 15.4;  DB 5;  Length 507;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    197 CGGGGTCTTCTCGTCTT 181


RESULT  45
AF153585/c
LOCUS       AF153585                 507 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya variegata 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF153585
VERSION     AF153585.1  GI:8885824
KEYWORDS    .
SOURCE      Mabuya variegata.
  ORGANISM  Mitochondrion Mabuya variegata
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (bases 1 to 507)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     First Data on the Molecular Phylogeography of Scincid Lizards of
            the Genus Mabuya
  JOURNAL   Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
   PUBMED   11020300
REFERENCE   2  (bases 1 to 507)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1999) Herpetology, Zoologisches
            Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, Bonn,
            NRW 53113, Germany
FEATURES             Location/Qualifiers
     source          1. .507
                     /organism="Mabuya variegata"
                     /organelle="mitochondrion"
                     /db_xref="taxon:111193"
     rRNA            <1. .>507
                     /product="16S ribosomal RNA"
BASE COUNT      169 a    127 c     98 g    113 t
ORIGIN


  Query Match           90.6%;  Score 15.4;  DB 5;  Length 507;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    197 CGGGGTCTTCTCGTCTT 181


RESULT  46
AF153566/c
LOCUS       AF153566                 508 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya cf. dumasi 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF153566
VERSION     AF153566.1  GI:8885805
KEYWORDS    .
SOURCE      Mabuya cf. dumasi.
  ORGANISM  Mitochondrion Mabuya cf. dumasi
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     First Data on the Molecular Phylogeography of Scincid Lizards of
            the Genus Mabuya
  JOURNAL   Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
   PUBMED   11020300
REFERENCE   2  (bases 1 to 508)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1999) Herpetology, Zoologisches
            Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, Bonn,
            NRW 53113, Germany
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="Mabuya cf. dumasi"
                     /organelle="mitochondrion"
                     /db_xref="taxon:96434"
     rRNA            <1. .>508
                     /product="16S ribosomal RNA"
BASE COUNT      161 a    135 c    100 g    112 t
ORIGIN


  Query Match           90.6%;  Score 15.4;  DB 5;  Length 508;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    195 CGGGGTCTTCTCGTCTT 179


RESULT  47
AF153568/c
LOCUS       AF153568                 508 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya elegans country Madagascar 16S ribosomal RNA gene, partial
            sequence; mitochondrial gene for mitochondrial product.
ACCESSION   AF153568
VERSION     AF153568.1  GI:8885807
KEYWORDS    .
SOURCE      Mabuya elegans.
  ORGANISM  Mitochondrion Mabuya elegans
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     First Data on the Molecular Phylogeography of Scincid Lizards of
            the Genus Mabuya
  JOURNAL   Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
   PUBMED   11020300
REFERENCE   2  (bases 1 to 508)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1999) Herpetology, Zoologisches
            Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, Bonn,
            NRW 53113, Germany
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="Mabuya elegans"
                     /organelle="mitochondrion"
                     /db_xref="taxon:96428"
                     /country="Madagascar: Kirindy"
     rRNA            <1. .>508
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BASE COUNT      160 a    131 c    102 g    115 t
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  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
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Qy      1 cggggtcttcccgtctt 17
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Db    198 CGGGGTCTTCTCGTCTT 182


RESULT  48
AF153581/c
LOCUS       AF153581                508 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya striata striata 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF153581
VERSION     AF153581.1  GI:8885820
KEYWORDS    .
SOURCE      Mabuya striata striata.
  ORGANISM  Mitochondrion Mabuya striata striata
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     First Data on the Molecular Phylogeography of Scincid Lizards of
            the Genus Mabuya
  JOURNAL   Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
   PUBMED   11020300
REFERENCE   2  (bases 1 to 508)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1999) Herpetology, Zoologisches
            Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, Bonn,
            NRW 53113, Germany
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="Mabuya striata striata"
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                     /sub_species="striata"
                     /db_xref="taxon:111288"
     rRNA            <1. .>508
                     /product="16S ribosomal RNA"
BASE COUNT      168 a    120 c    102 g    118 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 5;  Length 508;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    199 CGGGGTCTTCTCGTCTT 183


RESULT  49
AF153583/c
LOCUS       AF153583                508 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya sulcata 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF153583
VERSION     AF153583.1  GI:8885822
KEYWORDS    .
SOURCE      Mabuya sulcata.
  ORGANISM  Mitochondrion Mabuya sulcata
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     First Data on the Molecular Phylogeography of Scincid Lizards of
            the Genus Mabuya
  JOURNAL   Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
   PUBMED   11020300
REFERENCE   2  (bases 1 to 508)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1999) Herpetology, Zoologisches
            Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, Bonn,
            NRW 53113, Germany
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="Mabuya sulcata"
                     /organelle="mitochondrion"
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                     /product="16S ribosomal RNA"
BASE COUNT      170 a    126 c    101 g    111 t
ORIGIN


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  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    198 CGGGGTCTTCTCGTCTT 182


RESULT  50
AF153567/c
LOCUS       AF153567                509 bp    DNA     linear   VRT 06-NOV-2000
DEFINITION  Mabuya elegans 16S ribosomal RNA gene, partial sequence;
            mitochondrial gene for mitochondrial product.
ACCESSION   AF153567
VERSION     AF153567.1  GI:8885806
KEYWORDS    .
SOURCE      Mabuya elegans.
  ORGANISM  Mitochondrion Mabuya elegans
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
            Scincidae; Mabuya.
REFERENCE   1  (bases 1 to 509)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     First Data on the Molecular Phylogeography of Scincid Lizards of
            the Genus Mabuya
  JOURNAL   Mol. Phylogenet. Evol. 17 (1), 11-14 (2000)
   PUBMED   11020300
REFERENCE   2  (bases 1 to 509)
  AUTHORS   Mausfeld,P., Vences,M., Schmitz,A. and Veith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1999) Herpetology, Zoologisches
            Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, Bonn,
            NRW 53113, Germany
FEATURES             Location/Qualifiers
     source          1. .509
                     /organism="Mabuya elegans"
                     /organelle="mitochondrion"
                     /db_xref="taxon:96428"
     rRNA            <1. .>509
                     /product="16S ribosomal RNA"
BASE COUNT      161 a    131 c    103 g    114 t
ORIGIN


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  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    199 CGGGGTCTTCTCGTCTT 183
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:42:10 ; Search time 264.9 Seconds
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Title: US-09-673-645A-1
Perfect score: 17
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

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Post-processing: Minimum Match 0%
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Listing first 50 summaries

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24: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		17	100.0	17	21	AAZ44467	H. pylori 23S rRNA
2		15.4	90.6	17	21	AAZ44469	H. pylori 23S rRNA
3		15.4	90.6	17	21	AAZ44470	H. pylori 23S rRNA
4	c	15.4	90.6	67	18	AAV79232	Staphylococcus aur
5	c	15.4	90.6	86	22	AAC83429	E. coli target seq
6		15.4	90.6	600	23	AAS87235	DNA encoding novel
7	c	15.4	90.6	638	22	AAC89401	E.coli 23S rRNA DN
8		15.4	90.6	813	23	AAS82419	DNA encoding novel
9	c	15.4	90.6	2115	23	AAS77887	DNA encoding novel
10		15.4	90.6	2607	23	AAS87563	DNA encoding novel
11	c	15.4	90.6	2896	21	AAA99892	Escherichia coli 2
12		15.4	90.6	2904	21	AAA66047	E. coli proliferat
13		15.4	90.6	2904	21	AAA66052	E. coli proliferat
14	c	15.4	90.6	2904	22	AAH75411	E. coli 23S rRNA.
15	c	15.4	90.6	2904	22	AAF23016	E. coli 23S rRNA s
16	c	15.4	90.6	2904	22	AAC89403	Sequences from 23S
17	c	15.4	90.6	2907	19	AAV38096	Enterohaemorrhagic
18	c	15.4	90.6	2907	19	AAV38107	Enterohaemorrhagic
19		15.4	90.6	3084	23	AAS87233	DNA encoding novel
20	c	15.4	90.6	3118	22	AAH49806	Escherichia coli t
21	c	15.4	90.6	3740	15	AAQ54682	Potato sucrose pho
22	c	15.4	90.6	5013	20	AAX24985	E. coli MG1655 rrn
23	c	15.4	90.6	5014	20	AAX24987	E. coli MG1655 rrn
24		15.4	90.6	5090	20	AAX24988	E. coli MG1655 rrn
25	c	15.4	90.6	5097	20	AAX24983	E. coli MG1655 rrn
26	c	15.4	90.6	5098	20	AAX24984	E. coli MG1655 rrn
27	c	15.4	90.6	5105	20	AAX24989	E. coli MG1655 rrn
28		15.4	90.6	5341	20	AAX24986	E. coli MG1655 rrn
29	c	14.4	84.7	435	21	AAA81793	N. meningitidis pa
30	c	14.4	84.7	473	22	AAI91211	Human polynucleoti
31	c	14.4	84.7	509	20	AAX21151	Polynucleotide seq
32		14.4	84.7	597	21	AAA81810	N. meningitidis pa
33	c	14.4	84.7	650	21	AAF12552	Aspergillus oryzae
34	c	14.4	84.7	741	21	AAC43891	Arabidopsis thalia
35	c	14.4	84.7	1065	23	AAS54060	Pseudomonas aerugi
36	c	14.4	84.7	1430	21	AAC60039	Human secreted pro
37	c	14.4	84.7	1442	22	AAH90047	Human bone marrow
38	c	14.4	84.7	1593	22	AAH90100	Human bone marrow
39	c	14.4	84.7	1725	20	AAX22111	Human secreted pro
40		14.4	84.7	1902	23	ABL11755	Drosophila melanog
41	c	14.4	84.7	2061	20	AAV72295	Human blood bacter
42	c	14.4	84.7	2222	22	AAH89934	Human bone marrow
43	c	14.4	84.7	2542	20	AAV72294	Human blood bacter
44	c	14.4	84.7	3166	21	AAC76013	Human ORFX ORF1568
45	c	14.4	84.7	3398	20	AAX20282	Borrelia burgdorfe
46	c	14.4	84.7	5273	20	AAX24982	Haemophilus influe
47	c	14.4	84.7	5519	20	AAX24981	Haemophilus influe
48		14.4	84.7	5669	21	AAA81533	N. meningitidis pa
49	c	14.4	84.7	6585	21	AAA60446	Murine factor V en
50		14.4	84.7	7889	23	ABL11754	Drosophila melanog

ALIGNMENTS

RESULT 1
AAZ44467
ID AAZ44467 standard; DNA; 17 BP.
XX
AC AAZ44467;
XX
DT 06-APR-2000 (first entry)
XX
DE H. pylori 23S rRNA probe ClaR1.
XX
KW 23s rRNA; detection; antibiotic resistance; pathogen; probe; ss.
XX
OS Helicobacter pylori.
XX
PN DE19916610-A1.
XX
PD 25-NOV-1999.
XX
PF 13-APR-1999; 99DE-1016610.
XX
PR 22-MAY-1998; 98DE-1023098.
XX
PA (CREA-) CREATOGEN BIOSCIENCES GMBH.
XX
PI Haas R, Trebesius K, Apfel H;
XX
DR WPI; 2000-040346/04.

XX
PT Detecting antibiotic resistance in microorganisms by in situ
PT characterization of probes -
XX
PS Claim 18; Page 23; 28pp; German.
XX
CC This invention describes a novel method for detecting antibiotic
CC resistance in microorganisms by in situ characterization of a probe
CC hybridizing with an antibiotic resistance associated nucleic acid in
CC a microorganism. The method is used to test slow growing and/or in
CC vitro difficult or non cultivatable pathogens, e.g. Helicobacter pylori,
CC Mycobacteria, Porphyromonas gigivalis, Propionibacterium acnes, Borrelia
CC burgdorferi, Mycoplasma, Chlamydia, Tropheryma whippelii, Bartonella
CC legionella, Norkardia and Actinomycetes. The sample can be prepared from
CC human or animal tissue or body fluids. The method is used to test
CC samples that have no previous preparation for the microorganism in
CC question. In particular the method is used to detect antibiotic
CC resistance against in bacteria and protozoa. AAZ44467-Z444?4 represent
CC probes used in the method of the invention.
XX
SQ Sequence 17 BP; 0 A; 6 C; 5 G; 6 T; 0 other;

Query Match 100.0%; Score 17; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 cggggtcttcccgtctt 17

RESULT 2
AAZ44469
ID AAZ44469 standard; DNA; 17 BP.
XX
AC AAZ44469;
XX
DT 06-APR-2000 (first entry)
XX
DE H. pylori 23S rRNA probe ClaR3.
XX
KW 23s rRNA; detection; antibiotic resistance; pathogen; probe; ss.
XX
OS Helicobacter pylori.
XX
PN DE19916610-A1.
XX
PD 25-NOV-1999.
XX
PF 13-APR-1999; 99DE-1016610.
XX
PR 22-MAY-1998; 98DE-1023098.
XX
PA (CREA-) CREATOGEN BIOSCIENCES GMBH.
XX
PI Haas R, Trebesius K, Apfel H;
XX
DR WPI; 2000-040346/04.
XX
PT Detecting antibiotic resistance in microorganisms by in situ
PT characterization of probes -
XX
PS Claim 18; Page 23; 28pp; German.
XX
CC This invention describes a novel method for detecting antibiotic
CC resistance in microorganisms by in situ characterization of a probe
CC hybridizing with an antibiotic resistance associated nucleic acid in
CC a microorganism. The method is used to test slow growing and/or in
CC vitro difficult or non cultivatable pathogens, e.g. Helicobacter pylori,
CC Mycobacteria, Porphyromonas gigivalis, Propionibacterium acnes, Borrelia
CC burgdorferi, Mycoplasma, Chlamydia, Tropheryma whippelii, Bartonella
CC legionella, Norkardia and Actinomycetes. The sample can be prepared from
CC human or animal tissue or body fluids. The method is used to test
CC samples that have no previous preparation for the microorganism in
CC question. In particular the method is used to detect antibiotic
CC resistance against in bacteria and protozoa. AAZ44467-Z44474 represent
CC probes used in the method of the invention.
XX
SQ Sequence 17 BP; 0 A; 5 C; 6 G; 6 T; 0 other;

Query Match 90.6%; Score 15.4; DB 21; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 cggggtcttgcccgtctt 17

RESULT 3
AAZ44470
ID AAZ44470 standard; DNA; 17 BP.
XX
AC AAZ44470;
XX
DT 06-APR-2000 (first entry)
XX
DE H. pylori 23S rRNA probe ClaWT.
XX
KW 23s rRNA; detection; antibiotic resistance; pathogen; probe; ss.
XX
OS Helicobacter pylori.
XX
PN DE19916610-A1.
XX
PD 25-NOV-1999.
XX
PF 13-APR-1999; 99DE-1016610.
XX
PR 22-MAY-1998; 98DE-1023098.
XX
PA (CREA-) CREATOGEN BIOSCIENCES GMBH.
XX
PI Haas R, Trebesius K, Apfel H;
XX
DR WPI; 2000-040346/04.
XX
PT Detecting antibiotic resistance in microorganisms by in situ
PT characterization of probes -
XX
PS Claim 20; Page 23; 28pp; German.
XX
CC This invention describes a novel method for detecting antibiotic
CC resistance in microorganisms by in situ characterization of a probe
CC hybridizing with an antibiotic resistance associated nucleic acid in
CC a microorganism. The method is used to test slow growing and/or in
CC vitro difficult or non cultivatable pathogens, e.g. Helicobacter pylori,
CC Mycobacteria, Porphyromonas gigivalis, Propionibacterium acnes, Borrelia
CC burgdorferi, Mycoplasma, Chlamydia, Tropheryma whippelii, Bartonella
CC legionella, Norkardia and Actinomycetes. The sample can be prepared from
CC human or animal tissue or body fluids. The method is used to test
CC samples that have no previous preparation for the microorganism in
CC question. In particular the method is used to detect antibiotic
CC resistance against in bacteria and protozoa. AAZ44467-Z44474 represent
CC probes used in the method of the invention.
XX
SQ Sequence 17 BP; 0 A; 5 C; 5 G; 7 T; 0 other;

Query Match 90.6%; Score 15.4; DB 21; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17

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          ||||||||| |||||||
Db      1 cggggtctttccgtctt 17


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ID   AAV79232 standard; DNA; 67 BP.
XX
AC   AAV79232;
XX
DT   16-MAR-1999  (first entry)
XX
DE   Staphylococcus aureus contig SEQ ID #4921.
XX
KW   Computer readable medium; vaccine; S.aureus infection; immunodetection;
KW   cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KW   skin infection; surgical wound infection; scalded skin syndrome;
KW   toxic shock syndrome; ds.
XX
OS   Staphylococcus aureus.
XX
PN   EP786519-A2.
XX
PD   30-JUL-1997.
XX
PF   07-JAN-1997;   97EP-0100117.
XX
PR   05-JAN-1996;   96US-0009861.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Barash SC,  Choi GH,  Dillon PJ,  Fannon MR,  Kunsch CA;
PI   Rosen CA;
XX
DR   WPI; 1997-374922/35.
XX
PT   Polynucleotide(s) and proteins derived from Staphylococcus aureus  -
PT   stored on computer readable medium and used in the production of
PT   anti-S.aureus vaccines
XX
PS   Claim 1; Page 3122; 3271pp; English.
XX
CC   This sequence represents one of 5191 Staphylococcus aureus DNA sequences
CC   of the invention. The DNA sequences are recorded on a computer readable
CC   medium, preferably selected from a floppy or hard disk, random access
CC   memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC   the S.aureus DNA sequences allows putative functions to be assigned so
CC   that protein-encoding or regulatory regions of commercial, therapeutic or
CC   industrial importance can be obtained. Specifically, sequences which are
CC   likely to encode antigens have been identified and these polypeptides can
CC   be used in a vaccine composition against S.aureus infection. The
CC   polypeptides can also be used in a kit for the immunodetection of
CC   S.aureus in a sample. S.aureus is implicated in numerous human diseases,
CC   including cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC   skin and surgical wound infections, scalded skin syndrome, toxic shock
CC   syndrome, etc. Organisms transformed with the DNA sequences can be used
CC   for recombinant production of the polypeptides. The new DNA sequences
CC   (and their fragments) are useful as primers or probes for isolating
CC   homologues of any of the S.aureus DNA sequences contained on the
CC   computer readable medium.
XX
SQ   Sequence 67 BP; 22 A; 16 C; 16 G; 13 T; 0 other;


  Query Match            90.6%;  Score 15.4;  DB 18;  Length 67;
  Best Local Similarity   94.1%;  Pred. No. 1.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db     54 CGGGGTCTTTCCGTCTT 38


RESULT   5
AAC83429/c
ID   AAC83429 standard; RNA; 86 BP.
XX
AC   AAC83429;
XX
DT   27-FEB-2001  (first entry)
XX
DE   E. coli target sequence.
XX
KW   Probe; detection; rRNA; ss.
XX
OS   Escherichia coli.
XX
PN   WO200066786-A2.
XX
PD   09-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US12243.
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PR   03-MAY-1999;   99US-0132412.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Hogan JJ,  Gordon P;
XX
DR   WPI; 2001-007238/01.
XX
PT   Oligonucleotide probes useful for detecting and identifying rRNA or
PT   rDNA of Actinomycetes bacteria -
XX
PS   Disclosure; Fig 1; 44pp; English.
XX
CC   The present invention relates to an oligonucleotide probe that
CC   hybridizes to an Actinomycetes nucleic acid region corresponding to
CC   Escherichia coli rRNA nucleotide positions 1986-2064 to form a
CC   detectable probe/target duplex. The invention is useful for detecting
CC   the presence of Actinomycetes in a test sample. The test is specific
CC   and does not cross react with rRNA from numerous bacterial and fungal
CC   species.
XX
SQ   Sequence 86 BP; 22 A; 25 C; 25 G; 14 U; 0 other;


  Query Match            90.6%;  Score 15.4;  DB 22;  Length 86;
  Best Local Similarity   94.1%;  Pred. No. 1.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db     85 CGGGGTCTTTCCGTCTT 69


RESULT   6
AAS87235
ID   AAS87235 standard; cDNA; 600 BP.
XX
AC   AAS87235;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #23039.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
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XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG23048.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 23039; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 600 BP; 137 A; 179 C; 141 G; 143 T; 0 other;

Query Match 90.6%; Score 15.4; DB 23; Length 600;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||| |||||||
Db 397 cggggtctttccgtctt 413

RESULT 7
AAC89401/c
ID AAC89401 standard; DNA; 638 BP.
XX
AC AAC89401;
XX
DT 08-MAR-2001 (first entry)
XX
DE E.coli 23S rRNA DNA.
XX
KW 23S rRNA; ribosomal polynucleotide; infection; otitis media;
KW conjunctivitis; pneumonia; bacteremia; meningitis; sinusitis;
KW pleural empyema; endocarditis; ds.
XX
OS Escherichia coli.
XX
PN WO200071560-A1.
XX
PD 30-NOV-2000.
XX
PF 04-MAY-2000; 2000WO-US12133.
XX
PR 20-MAY-1999; 99US-0134973.
PR 07-JUN-1999; 99US-0137837.
PR 14-JUN-1999; 99US-0139095.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Hegg LA, Sterner TA;
XX
DR WPI; 2001-102280/11.
XX
PT Novel bacterial ribosomal polynucleotides useful for identifying
PT agonists and antagonists for treating otitis media, conjunctivitis,
PT pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and
PT endocarditis -
XX
PS Claim 1; Page 16; 67pp; English.
XX
CC The present invention relates to Escherichia coli 23S rRNA.
CC Derivatives from this protein may be useful for treating an
CC individual having a need to inhibit a ribosomal polynucleotide.
CC Agonists and antagonists identified are useful for treating an
CC individual infected by Staphylococcus aureus or Streptococcus
CC pneumoniae. The DNA sequence may also be used in the
CC discovery and screening of antibacterial drugs, and its respective
CC mRNA may be used to construct antisense sequences to control the
CC expression of the coding sequence of interest. The agonists and
CC antagonists are useful for treating otitis media, conjunctivitis,
CC pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and
CC endocarditis.
XX
SQ Sequence 638 BP; 149 A; 140 C; 202 G; 147 T; 0 other;

Query Match 90.6%; Score 15.4; DB 22; Length 638;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||| |||||||
Db 97 CGGGGTCTTTCCGTCTT 81

RESULT 8
AAS82419
ID AAS82419 standard; cDNA; 813 BP.
XX
AC AAS82419;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #18223.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.

DR P-PSDB; ABG18232.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 18223; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 813 BP; 200 A; 234 C; 187 G; 192 T; 0 other;

Query Match 90.6%; Score 15.4; DB 23; Length 813;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||| |||||||
Db 610 cggggtctttccgtctt 626

RESULT 9
AAS77887/c
ID AAS77887 standard; cDNA; 2115 BP.
XX
AC AAS77887;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #13691.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG13700.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 13691; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2115 BP; 389 A; 652 C; 728 G; 346 T; 0 other;

Query Match 90.6%; Score 15.4; DB 23; Length 2115;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||| |||||||
Db 144 CGGGGTCTTTCCGTCTT 128

RESULT 10
AAS87563
ID AAS87563 standard; cDNA; 2607 BP.
XX
AC AAS87563;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #23367.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG23376.
XX

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 23367; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2607 BP; 622 A; 707 C; 658 G; 620 T; 0 other;

Query Match 90.6%; Score 15.4; DB 23; Length 2607;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||| |||||||
Db 2404 cggggtctttccgtctt 2420

RESULT 11
AAA99892/c
ID AAA99892 standard; DNA; 2896 BP.
XX
AC AAA99892;
XX
DT 15-FEB-2001 (first entry)
XX
DE Escherichia coli 23S gene.
XX
KW Johne's disease; Crohn's disease; subspecies detection; 23S rRNA; ds.
XX
OS Escherichia coli.
XX
PN WO200034517-A1.
XX
PD 15-JUN-2000.
XX
PF 03-DEC-1999; 99WO-NL00741.
XX
PR 04-DEC-1998; 98EP-0204117.
XX
PA (MICR-) MICROSCREEN BV.
PA (GEZO-) GEZONDHEIDSDIENST DIEREN.
XX
PI Schut F, Ensing HZ, Koopmans HH, Tan PST, Wagter LHA;
PI Brinkhof JMA, Van Maanen C;
XX
DR WPI; 2000-423446/36.
XX
PT Detection of Mycobacterium avium paratuberculosis by identification of
PT specific 23S rRNA mutations at positions 754, 1363 or 3093 useful for
PT diagnosis of Johne's disease -
XX
PS Claim 4; Fig 2; 81pp; English.
XX
CC The present sequence is the Esherichia coli 23S rRNA gene. This sequence
CC contains several mutations when compared to the Mycobacterium avium
CC subspecies paratuberculosis, and some are unique enough to allow the
CC development of a probe which enables specific identification of the
CC presence of paratuberculosis. The organism is responsible for Johne's
CC disease in ruminants, especially cows, and is possibly transmitted to
CC humans where it may lead to Crohn's disease. Efficient detection of the
CC bacterium, using a probe designed using its rRNA gene, can be used to
CC identify infected animals so that they can be removed from the herd and
CC destroyed.
XX
SQ Sequence 2896 BP; 761 A; 638 C; 908 G; 589 T; 0 other;

Query Match 90.6%; Score 15.4; DB 21; Length 2896;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||| |||||||
Db 2069 CGGGGTCTTTCCGTCTT 2053

RESULT 12
AAA66047
ID AAA66047 standard; DNA; 2904 BP.
XX
AC AAA66047;
XX
DT 05-OCT-2000 (first entry)
XX
DE E. coli proliferation associated coding sequence SEQ ID NO:239.
XX
KW Escherichia coli; E. coli; proliferation; inhibition; screening;
KW antimicrobial; bacterial growth; antisense therapy; antibacterial; ds.
XX
OS Escherichia coli.
XX
PN WO200044906-A2.
XX
PD 03-AUG-2000.
XX
PF 27-JAN-2000; 2000WO-US02200.
XX
PR 27-JAN-1999; 99US-0117405.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Zyskind J, Ohlsen KL, Trawick J, Forsyth RA, Froelich JM, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2000-514822/46.
XX
PT Novel polynucleotides and polypeptides associated with microorganism
PT proliferation, used to identify inhibitors of bacterial growth and
PT proliferation, for use in antisense therapy -
XX
PS Claim 8; Page 172-173; 316pp; English.
XX
CC AAA65809 to AAA65889 and AAA66058 to AAA66138 represent nucleotide
CC sequences derived from Escherichia coli which inhibit E. coli
CC proliferation. AAA65890 to AAA66055 and AAB15886 to AAB16040 represent
CC nucleotide and protein sequences associated with E. coli proliferation.
CC AAA66056 and AAA66057 represent primers used for sequencing E. coli
CC proliferation inhibiting nucleotide inserts in an example from the
CC present invention. Methods from the present invention can be used to
CC identify a proliferation- required gene in a microorganism, by contacting
CC a microorganism with a proliferation-required gene activity inhibitory
CC nucleic acid identified in another organism, and determining if

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CC   inhibition occurs in the second microorganism. The nucleic acid sequences
CC   identified as being required for bacterial growth and proliferation, can
CC   be used for antisense therapy for killing bacteria.
XX
SQ   Sequence 2904 BP; 591 A; 912 C; 639 G; 762 T; 0 other;


  Query Match             90.6%;  Score 15.4;  DB 21;  Length 2904;
  Best Local Similarity   94.1%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          |||||||||| |||||||
Db    838 cggggtctttccgtctt 854


RESULT  13
AAA66052
ID   AAA66052 standard; RNA; 2904 BP.
XX
AC   AAA66052;
XX
DT   05-OCT-2000  (first entry)
XX
DE   E. coli proliferation associated nucleotide sequence SEQ ID NO:399.
XX
KW   Escherichia coli; E. coli; proliferation; inhibition; screening;
KW   antimicrobial; bacterial growth; antisense therapy; antibacterial; ss.
XX
OS   Escherichia coli.
XX
PN   WO200044906-A2.
XX
PD   03-AUG-2000.
XX
PF   27-JAN-2000; 2000WO-US02200.
XX
PR   27-JAN-1999;   99US-0117405.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Zyskind J,  Ohlsen KL,  Trawick J,  Forsyth RA,  Froelich JM,  Carr GJ;
PI   Yamamoto RT,  Xu HH;
XX
DR   WPI; 2000-514822/46.
XX
PT   Novel polynucleotides and polypeptides associated with microorganism
PT   proliferation, used to identify inhibitors of bacterial growth and
PT   proliferation, for use in antisense therapy -
XX
PS   Example 3; Page 295-296; 316pp; English.
XX
CC   AAA65809 to AAA65889 and AAA66058 to AAA66138 represent nucleotide
CC   sequences derived from Escherichia coli which inhibit E. coli
CC   proliferation. AAA65890 to AAA66055 and AAB15886 to AAB16040 represent
CC   nucleotide and protein sequences associated with E. coli proliferation.
CC   AAA66056 and AAA66057 represent primers used for sequencing E. coli
CC   proliferation inhibiting nucleotide inserts in an example from the
CC   present invention. Methods from the present invention can be used to
CC   identify a proliferation- required gene in a microorganism, by contacting
CC   a microorganism with a proliferation-required gene activity inhibitory
CC   nucleic acid identified in another organism, and determining if
CC   inhibition occurs in the second microorganism. The nucleic acid sequences
CC   identified as being required for bacterial growth and proliferation, can
CC   be used for antisense therapy for killing bacteria.
XX
SQ   Sequence 2904 BP; 591 A; 912 C; 639 G; 762 U; 0 other;


  Query Match             90.6%;  Score 15.4;  DB 21;  Length 2904;
  Best Local Similarity   58.8%;  Pred. No. 1.4e+02;
  Matches   10;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          |||||:|:: |||:|::
Db    838 cggggucuuuccgucuu 854


RESULT  14
AAH75411/c
ID   AAH75411 standard; rRNA; 2904 BP.
XX
AC   AAH75411;
XX
DT   22-OCT-2001  (first entry)
XX
DE   E. coli 23S rRNA.
XX
KW   16S rRNA; 23S rRNA; RNA binding; antimicrobial; ss.
XX
OS   Escherichia coli.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1..8
FT                   /*tag=  a
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 2902-2895 to form a duplex"
FT   misc_binding    16..24
FT                   /*tag=  b
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 525-516 to form a duplex"
FT   misc_binding    30
FT                   /*tag=  c
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotide 510"
FT   misc_binding    31..32
FT                   /*tag=  d
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 474-473 to form a duplex"
FT   misc_binding    35..44
FT                   /*tag=  e
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 445-433 to form a duplex"
FT   misc_binding    54..56
FT                   /*tag=  f
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 116-114 to form a duplex"
FT   stem_loop       58..69
FT                   /*tag=  g
FT   stem_loop       76..110
FT                   /*tag=  h
FT   misc_binding    114..116
FT                   /*tag=  i
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 56-54 to form a duplex"
FT   stem_loop       121..130
FT                   /*tag=  j
FT   stem_loop       131..148
FT                   /*tag=  k
FT   stem_loop       150..176
FT                   /*tag=  l
FT   stem_loop       184..212
FT                   /*tag=  m
FT   stem_loop       224..231
FT                   /*tag=  n
FT   stem_loop       235..262
FT                   /*tag=  o
FT   misc_binding    265..268
FT                   /*tag=  p
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 427-424 to form a duplex"
FT   misc_binding    271..297
FT                   /*tag=  q
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 366-341 to form a duplex"
FT   stem_loop       301..316
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FT                   /*tag= r
FT   stem_loop       319..323
FT                   /*tag= s
FT   stem_loop       325..337
FT                   /*tag= t
FT   misc_binding    341..366
FT                   /*tag= u
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 297-271 to form a duplex"
FT   stem_loop       376..398
FT                   /*tag= v
FT   stem_loop       406..421
FT                   /*tag= w
FT   misc_binding    424..427
FT                   /*tag= x
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 268-265 to form a duplex"
FT   misc_binding    433..445
FT                   /*tag= y
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 44-35 to form a duplex"
FT   stem_loop       461..468
FT                   /*tag= z
FT   misc_binding    473..474
FT                   /*tag= aa
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 32-31 to form a duplex"
FT   stem_loop       484..496
FT                   /*tag= ab
FT   misc_binding    510
FT                   /*tag= ac
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotide 30"
FT   misc_binding    516..525
FT                   /*tag= ad
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 24-16 to form a duplex"
FT   stem_loop       533..560
FT                   /*tag= ae
FT   misc_binding    579..584
FT                   /*tag= af
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 1261-1256 to form a duplex"
FT   misc_binding    589..601
FT                   /*tag= ag
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 668-656 to form a duplex"
FT   stem_loop       604..624
FT                   /*tag= ah
FT   stem_loop       628..635
FT                   /*tag= ai
FT   stem_loop       638..650
FT                   /*tag= aj
FT   misc_binding    656..668
FT                   /*tag= ak
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 601-589 to form a duplex"
FT   misc_binding    671..672
FT                   /*tag= al
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 809-808 to form a duplex"
FT   misc_binding    678..683
FT                   /*tag= am
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 799-794 to form a duplex"
FT   misc_binding    687..698
FT                   /*tag= an
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 763-775 to form a duplex"
FT   stem_loop       700..732
FT                   /*tag= ao
FT   stem_loop       736..760
FT                   /*tag= ap
FT   protein_bind    752
FT                   /*tag= aq
FT                   /bound_moiety= "Vemamycin B"
FT   misc_binding    763..775
FT                   /*tag= ar
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 698-687 to form a duplex"
FT   stem_loop       777..787
FT                   /*tag= as
FT   misc_binding    794..799
FT                   /*tag= at
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 683-678 to form a duplex"
FT   misc_binding    808..809
FT                   /*tag= au
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 672-671 to form a duplex"
FT   misc_binding    812..817
FT                   /*tag= av
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 1195-1190 to form a duplex"
FT   stem_loop       822..835
FT                   /*tag= aw
FT   stem_loop       838..940
FT                   /*tag= ax
FT   protein_bind    913
FT                   /*tag= ay
FT                   /bound_moiety= "Viomycin"
FT   protein_bind    914
FT                   /*tag= az
FT                   /bound_moiety= "Viomycin"
FT   stem_loop       946..971
FT                   /*tag= ba
FT   stem_loop       976..987
FT                   /*tag= bb
FT   misc_binding    991..998
FT                   /*tag= bc
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 1163-1157 to form a duplex"
FT   misc_binding    1002..1004
FT                   /*tag= bd
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 1153-1151 to form a duplex"
FT   misc_binding    1011..1019
FT                   /*tag= be
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 1150-1143 to form a duplex"
FT   misc_binding    1030..1043
FT                   /*tag= bf
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 1124-1112 to form a duplex"
FT   misc_feature    1031..1123
FT                   /*tag= bg
FT                   /label= "GTPase Centre"
FT   misc_binding    1052..1055
FT                   /*tag= bh
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 1107-1104 to form a duplex"
FT   stem_loop       1057..1081
FT                   /*tag= bi
FT   protein_bind    1067

  Query Match             90.6%;  Score 15.4;  DB 22;  Length 2904;
  Best Local Similarity   94.1%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtctt 17
           ||||||||| |||||||
Db    2068 CGGGGTCTTTCCGTCTT 2052


RESULT  15
AAF23016/c
```

ID AAF23016 standard; rRNA; 2904 BP.
XX
AC AAF23016;
XX
DT 20-MAR-2001 (first entry)
XX
DE E. coli 23S rRNA sequence.
XX
KW Probe; PCR primer; 5S rRNA; 16S rRNA; 23S rRNA; 28S rRNA; 18S rRNA;
KW Mycobacterium; Enterococcus; Chlamydia; Mycoplasma; E. coli; Legionella;
KW Salmonella; Pseudomonas; Campylobacter; Neisseria gonorrheae; fungus;
KW bacterium; ss.
XX
OS Escherichia coli.
XX
PN US6150517-A.
XX
PD 21-NOV-2000.
XX
PF 30-MAY-1995; 95US-0454063.
XX
PR 22-FEB-1994; 94US-0200866.
PR 24-NOV-1987; 87US-0295208.
PR 24-NOV-1987; 87WO-US03009.
PR 11-DEC-1991; 91US-0806929.
PR 24-NOV-1986; 86US-0934244.
PR 07-AUG-1987; 87US-0083542.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI McDonough SH, Kop JA, Smith RD, Hogan JJ;
XX
DR WPI; 2001-060029/07.
XX
PT Preparing a probe for nucleic acid hybridization assays comprises
PT constructing a nucleotide polymer sufficiently complementary to
PT hybridize to an rRNA region that distinguishes non-viral target from
PT non-viral non-target species -
XX
PS Disclosure; Fig 2; 75pp; English.
XX
CC The present invention provides novel methods of producing probes for use
CC in the identification of a number of microorganisms. These include E.
CC coli, Mycobacteria, Mycoplasma, Campylobacter, Chlamydia, Enterobacter,
CC Legionella, Salmonella, Pseudomonas, Neisseria gonorrheae, fungi and
CC bacteria.
XX
SQ Sequence 2904 BP; 762 A; 639 C; 912 G; 591 U; 0 other;

Query Match 90.6%; Score 15.4; DB 22; Length 2904;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||| |||||||
Db 2067 CGGGGTCTTTCCGTCTT 2051

RESULT 16
AAC89403/c
ID AAC89403 standard; DNA; 2904 BP.
XX
AC AAC89403;
XX
DT 08-MAR-2001 (first entry)
XX
DE Sequences from 23S E.coli ribosomal RNA.
XX
KW 23S rRNA; ribosomal polynucleotide; infection; otitis media;
KW conjunctivitis; pneumonia; bacteremia; meningitis; sinusitis;
KW pleural empyema; endocarditis; ds.
XX
OS Escherichia coli.
XX
PN WO200071560-A1.
XX
PD 30-NOV-2000.
XX
PF 04-MAY-2000; 2000WO-US12133.
XX
PR 20-MAY-1999; 99US-0134973.
PR 07-JUN-1999; 99US-0137837.
PR 14-JUN-1999; 99US-0139095.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Hegg LA, Sterner TA;
XX
DR WPI; 2001-102280/11.
XX
PT Novel bacterial ribosomal polynucleotides useful for identifying
PT agonists and antagonists for treating otitis media, conjunctivitis,
PT pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and
PT endocarditis -
XX
PS Claim 10; Page 18-19; 67pp; English.
XX
CC The present invention relates to Escherichia coli 23S rRNA.
CC Derivatives from this protein may be useful for treating an
CC individual having a need to inhibit a ribosomal polynucleotide.
CC Agonists and antagonists identified are useful for treating an
CC individual infected by Staphylococcus aureus or Streptococcus
CC pneumoniae. The DNA sequence may also be used in the
CC discovery and screening of antibacterial drugs, and its respective
CC mRNA may be used to construct antisense sequences to control the
CC expression of the coding sequence of interest. The agonists and
CC antagonists are useful for treating otitis media, conjunctivitis,
CC pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and
CC endocarditis.
XX
SQ Sequence 2904 BP; 762 A; 639 C; 912 G; 591 T; 0 other;

Query Match 90.6%; Score 15.4; DB 22; Length 2904;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||| |||||||
Db 2067 CGGGGTCTTTCCGTCTT 2051

RESULT 17
AAV38096/c
ID AAV38096 standard; DNA; 2907 BP.
XX
AC AAV38096;
XX
DT 15-SEP-1998 (first entry)
XX
DE Enterohaemorrhagic E. coli 0157 23A rRNA gene DNA sequence.
XX
KW Enterohaemorrhagic; Escherichia coli 0157; 23S rRNA; hybridisation;
KW probe; detection; diagnosis; infection; PCR primer; ds.
XX
OS Escherichia coli.
XX
PN JP10165182-A.
XX
PD 23-JUN-1998.
XX
PF 09-DEC-1996; 96JP-0328837.
XX
PR 09-DEC-1996; 96JP-0328837.

XX
PA (NIFL-) NIPPON FLOUR MILLS CO LTD.
PA (ZENK-) ZENKOKU NOGYO KYODO KUMIAI RENGOKAI.
XX
DR WPI; 1998-416777/36.
XX
PT Hybridisation probe derived from 23S ribosomal RNA of
PT enterohaemorrhagic E. coli O157 - or the gene encoding the 23S
PT ribosomal RNA; used for the specific detection of enterohaemorrhagic
PT E. coli O157
XX
PS Example 2; Page 5-6; 18pp; Japanese.
XX
CC A method has been developed for the detection of enterohaemorrhagic
CC Escherichia coli (EHEC) O157 in which nucleic acid fragments of the
CC 23S ribosomal RNA (rRNA) gene from EHEC 0157 are used as hybridisation
CC probes. The present sequence represents the 23S rRNA gene from EHEC 0157
CC from the present invention. Probes from the present invention can be
CC labelled and used as hybridisation probes to detect EHEC 0157 in a
CC sample. They can specifically detect E. coli O157 and hence diagnose
CC infection.
XX
SQ Sequence 2907 BP; 760 A; 638 C; 909 G; 592 T; 8 other;

Query Match 90.6%; Score 15.4; DB 19; Length 2907;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||| |||||||
Db 2070 CGGGGTCTTTCCGTCTT 2054

RESULT 18
AAV38107/c
ID AAV38107 standard; rRNA; 2907 BP.
XX
AC AAV38107;
XX
DT 15-SEP-1998 (first entry)
XX
DE Enterohaemorrhagic E. coli 0157 23A rRNA gene rRNA sequence.
XX
KW Enterohaemorrhagic; Escherichia coli 0157; 23S rRNA; hybridisation;
KW probe; detection; diagnosis; infection; PCR primer; ss.
XX
OS Escherichia coli.
XX
PN JP10165182-A.
XX
PD 23-JUN-1998.
XX
PF 09-DEC-1996; 96JP-0328837.
XX
PR 09-DEC-1996; 96JP-0328837.
XX
PA (NIFL-) NIPPON FLOUR MILLS CO LTD.
PA (ZENK-) ZENKOKU NOGYO KYODO KUMIAI RENGOKAI.
XX
DR WPI; 1998-416777/36.
XX
PT Hybridisation probe derived from 23S ribosomal RNA of
PT enterohaemorrhagic E. coli O157 - or the gene encoding the 23S
PT ribosomal RNA; used for the specific detection of enterohaemorrhagic
PT E. coli O157
XX
PS Disclosure; Page 4-5; 18pp; Japanese.
XX
CC A method has been developed for the detection of enterohaemorrhagic
CC Escherichia coli (EHEC) O157 in which nucleic acid fragments of the
CC 23S ribosomal RNA (rRNA) gene from EHEC 0157 are used as hybridisation
CC probes. The present sequence represents the 23S rRNA gene from EHEC 0157
CC from the present invention. Probes from the present invention can be
CC labelled and used as hybridisation probes to detect EHEC O157 in a
CC sample. They can specifically detect E. coli O157 and hence diagnose
CC infection.
XX
SQ Sequence 2907 BP; 760 A; 638 C; 909 G; 592 U; 8 other;

Query Match 90.6%; Score 15.4; DB 19; Length 2907;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||| |||||||
Db 2070 CGGGGTCTTTCCGTCTT 2054

RESULT 19
AAS87233
ID AAS87233 standard; cDNA; 3084 BP.
XX
AC AAS87233;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #23037.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG23046.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 23037; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.

```
  Query Match             90.6%;  Score 15.4;  DB 20;  Length 5014;
  Best Local Similarity   94.1%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db   3964 CGGGGTCTTTCCGTCTT 3948


RESULT  24
AAX24988
ID   AAX24988 standard; DNA; 5090 BP.
XX
AC   AAX24988;
XX
DT   05-JUL-1999  (first entry)
XX
DE   E. coli MG1655 rrnG operon (16S-spacer-23S-spacer-5S).
XX
KW   Speciation; ribotyping; species discrimination; marker; RFLP;
KW   restriction fragment length polymorphism; bacterium; fungus;
KW   pathogen; rrnG operon; 16S RNA gene; 23S RNA gene; ds.
XX
OS   Escherichia coli.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    complement (1..120)
FT                   /*tag=  a
FT                   /label= 5S
FT   misc_feature    complement (213..3116)
FT                   /*tag=  b
FT                   /label= 23S
FT   misc_feature    complement (3543..5090)
FT                   /*tag=  c
FT                   /label= 16S
XX
PN   WO9905325-A1.
XX
PD   04-FEB-1999.
XX
PF   24-JUL-1998;   98WO-US15464.
XX
PR   25-JUL-1997;   97US-0053097.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Goldstein RN;
XX
DR   WPI; 1999-142969/12.
XX
PT   Determining species of bacteria and fungi - useful for
PT   distinguishing between bacterial/fungal species, and for determining
PT   the identity of bacterial/fungal pathogens in biological samples
XX
PS   Disclosure; Fig 7 (53/67-56/67); 133pp; English.
XX
CC   This is the DNA sequence of the Escherichia coli strain MG1655
CC   rrnG operon (16S-spacer-23S-spacer-5S).  Restriction sites for
CC   enzymes cutting the operon 5 times or less have been determined.
CC   E. coli rrnA-rrnH operon sequences are provided (see AAX24983-89).
CC   Methods and compositions are described for determining the species
CC   of an unknown bacterium or fungus in a sample.  The method involves
CC   isolating and digesting bacterial (or fungal) DNA encoding 16S and
CC   23S rRNA from a sample with restriction enzymes, detecting the
CC   products, and comparing them to signature bands from a number of
CC   bacteria.  The method generates a species-conserved set of RFLP
CC   bands, unique for each species.  These species-conserved sets
CC   represent precise markers appopropriate for inter-species
CC   discriminatory purposes (i.e. to determine the species of a given,
CC   unknown isolate e.g. in a clinical specimen).  In contrast to
CC   conventional ribotyping, the present invention utilises the
CC   ribosomal operon sequences which vary less than 3% (and more
CC   preferably less than 2%) within a species and vary between species.
CC   The method is useful for medical, food, agricultural and
CC   environmental testing.  It does not require sequencing of nucleic
CC   acid from biological samples.
XX
SQ   Sequence 5090 BP; 1060 A; 1568 C; 1136 G; 1326 T; 0 other;


  Query Match             90.6%;  Score 15.4;  DB 20;  Length 5090;
  Best Local Similarity   94.1%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db   1050 cggggtctttccgtctt 1066


RESULT  25
AAX24983/c
ID   AAX24983 standard; DNA; 5097 BP.
XX
AC   AAX24983;
XX
DT   05-JUL-1999  (first entry)
XX
DE   E. coli MG1655 rrnA operon (16S-spacer-23S-spacer-5S).
XX
KW   Speciation; ribotyping; species discrimination; marker; RFLP;
KW   restriction fragment length polymorphism; bacterium; fungus;
KW   pathogen; rrnA operon; 16S RNA gene; 23S RNA gene; ds.
XX
OS   Escherichia coli.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..1547
FT                   /*tag=  a
FT                   /label= 16S
FT   misc_feature    1980..4884
FT                   /*tag=  b
FT                   /label= 23S
FT   misc_feature    4978..5097
FT                   /*tag=  c
FT                   /label= 5S
XX
PN   WO9905325-A1.
XX
PD   04-FEB-1999.
XX
PF   24-JUL-1998;   98WO-US15464.
XX
PR   25-JUL-1997;   97US-0053097.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Goldstein RN;
XX
DR   WPI; 1999-142969/12.
XX
PT   Determining species of bacteria and fungi - useful for
PT   distinguishing between bacterial/fungal species, and for determining
PT   the identity of bacterial/fungal pathogens in biological samples
XX
PS   Disclosure; Fig 7 (18/67-21/67); 133pp; English.
XX
CC   This is the DNA sequence of the Escherichia coli strain MG1655
CC   rrnA operon (16S-spacer-23S-spacer-5S).  Restriction sites for
CC   enzymes cutting the operon 5 times or less have been determined.
CC   E. coli rrnA-rrnH operon sequences are provided (see AAX24983-89).
CC   Methods and compositions are described for determining the species
CC   of an unknown bacterium or fungus in a sample.  The method involves
CC   isolating and digesting bacterial (or fungal) DNA encoding 16S and
CC   23S rRNA from a sample with restriction enzymes, detecting the
CC   products, and comparing them to signature bands from a number of
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CC   bacteria.  The method generates a species-conserved set of RFLP
CC   bands, unique for each species.  These species-conserved sets
CC   represent precise markers appopropriate for inter-species
CC   discriminatory purposes (i.e. to determine the species of a given,
CC   unknown isolate e.g. in a clinical specimen).  In contrast to
CC   conventional ribotyping, the present invention utilises the
CC   ribosomal operon sequences which vary less than 3% (and more
CC   preferably less than 2%) within a species and vary between species.
CC   The method is useful for medical, food, agricultural and
CC   environmental testing.  It does not require sequencing of nucleic
CC   acid from biological samples.
XX
SQ   Sequence 5097 BP; 1333 A; 1131 C; 1565 G; 1068 T; 0 other;


  Query Match             90.6%;  Score 15.4;  DB 20;  Length 509/;
  Best Local Similarity   94.1%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          |||||||||| |||||||
Db   4047 CGGGGTCTTTCCGTCTT 4031


RESULT  26
AAX24984/c
ID   AAX24984 standard; DNA; 5098 BP.
XX
AC   AAX24984;
XX
DT   05-JUL-1999  (first entry)
XX
DE   E. coli MG1655 rrnB operon (16S-spacer-23S-spacer-5S).
XX
KW   Speciation; ribotyping; species discrimination; marker; RFLP;
KW   restriction fragment length polymorphism; bacterium; fungus;
KW   pathogen; rrnB operon; 16S RNA gene; 23S RNA gene; ds.
XX
OS   Escherichia coli.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..1542
FT                   /*tag=  a
FT                   /label= 16S
FT   misc_feature    1983..4884
FT                   /*tag=  b
FT                   /label= 23S
FT   misc_feature    4979..5098
FT                   /*tag=  c
FT                   /label= 5S
XX
PN   WO9905325-A1.
XX
PD   04-FEB-1999.
XX
PF   24-JUL-1998;   98WO-US15464.
XX
PR   25-JUL-1997;   97US-0053097.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Goldstein RN;
XX
DR   WPI; 1999-142969/12.
XX
PT   Determining species of bacteria and fungi - useful for
PT   distinguishing between bacterial/fungal species, and for determining
PT   the identity of bacterial/fungal pathogens in biological samples
XX
PS   Disclosure; Fig 7 (25/67-28/67); 133pp; English.
XX
CC   This is the DNA sequence of the Escherichia coli strain MG1655
CC   rrnB operon (16S-spacer-23S-spacer-5S).  Restriction sites for
CC   enzymes cutting the operon 5 times or less have been determined.
CC   E. coli rrnA-rrnH operon sequences are provided (see AAX24983-89).
CC   Methods and compositions are described for determining the species
CC   of an unknown bacterium or fungus in a sample.  The method involves
CC   isolating and digesting bacterial (or fungal) DNA encoding 16S and
CC   23S rRNA from a sample with restriction enzymes, detecting the
CC   products, and comparing them to signature bands from a number of
CC   bacteria.  The method generates a species-conserved set of RFLP
CC   bands, unique for each species.  These species-conserved sets
CC   represent precise markers appopropriate for inter-species
CC   discriminatory purposes (i.e. to determine the species of a given,
CC   unknown isolate e.g. in a clinical specimen).  In contrast to
CC   conventional ribotyping, the present invention utilises the
CC   ribosomal operon sequences which vary less than 3% (and more
CC   preferably less than 2%) within a species and vary between species.
CC   The method is useful for medical, food, agricultural and
CC   environmental testing.  It does not require sequencing of nucleic
CC   acid from biological samples.
XX
SQ   Sequence 5098 BP; 1334 A; 1151 C; 1552 G; 1061 T; 0 other;


  Query Match             90.6%;  Score 15.4;  DB 20;  Length 5098;
  Best Local Similarity   94.1%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          |||||||||| |||||||
Db   4049 CGGGGTCTTTCCGTCTT 4033


RESULT  27
AAX24989/c
ID   AAX24989 standard; DNA; 5105 BP.
XX
AC   AAX24989;
XX
DT   05-JUL-1999  (first entry)
XX
DE   E. coli MG1655 rrnH operon (16S-spacer-23S-spacer-5S).
XX
KW   Speciation; ribotyping; species discrimination; marker; RFLP;
KW   restriction fragment length polymorphism; bacterium; fungus;
KW   pathogen; rrnH operon; 16S RNA gene; 23S RNA gene; ds.
XX
OS   Escherichia coli.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..1542
FT                   /*tag=  a
FT                   /label= 16S
FT   misc_feature    1989..4892
FT                   /*tag=  b
FT                   /label= 23S
FT   misc_feature    4885..5105
FT                   /*tag=  c
FT                   /label= 5S
XX
PN   WO9905325-A1.
XX
PD   04-FEB-1999.
XX
PF   24-JUL-1998;   98WO-US15464.
XX
PR   25-JUL-1997;   97US-0053097.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Goldstein RN;
XX
DR   WPI; 1999-142969/12.
XX
PT   Determining species of bacteria and fungi - useful for
```

```
PT   distinguishing between bacterial/fungal species, and for determining
PT   the identity of bacterial/fungal pathogens in biological samples
XX
PS   Disclosure; Fig 7 (60/67-63/67); 133pp; English.
XX
CC   This is the DNA sequence of the Escherichia coli strain MG1655
CC   rrnH operon (16S-spacer-23S-spacer-5S).  Restriction sites for
CC   enzymes cutting the operon 5 times or less have been determined.
CC   E. coli rrnA-rrnH operon sequences are provided (see AAX24983-89).
CC   Methods and compositions are described for determining the species
CC   of an unknown bacterium or fungus in a sample.  The method involves
CC   isolating and digesting bacterial (or fungal) DNA encoding 16S and
CC   23S rRNA from a sample with restriction enzymes, detecting the
CC   products, and comparing them to signature bands from a number of
CC   bacteria.  The method generates a species-conserved set of RFLP
CC   bands, unique for each species.  These species-conserved sets
CC   represent precise markers appopropriate for inter-species
CC   discriminatory purposes (i.e. to determine the species of a given,
CC   unknown isolate e.g. in a clinical specimen).  In contrast to
CC   conventional ribotyping, the present invention utilises the
CC   ribosomal operon sequences which vary less than 3% (and more
CC   preferably less than 2%) within a species and vary between species.
CC   The method is useful for medical, food, agricultural and
CC   environmental testing.  It does not require sequencing of nucleic
CC   acid from biological samples.
XX
SQ   Sequence 5105 BP; 1334 A; 1133 C; 1569 G; 1069 T; 0 other;

  Query Match             90.6%;  Score 15.4;  DB 20;  Length 5105;
  Best Local Similarity   94.1%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db   4055 CGGGGTCTTTCCGTCTT 4039


RESULT  28
AAX24986
ID   AAX24986 standard; DNA; 5341 BP.
XX
AC   AAX24986;
XX
DT   05-JUL-1999  (first entry)
XX
DE   E. coli MG1655 rrnD operon (16S-spacer-23S-spacer-5S).
XX
KW   Speciation; ribotyping; species discrimination; marker; RFLP;
KW   restriction fragment length polymorphism; bacterium; fungus;
KW   pathogen; rrnD operon; 16S RNA gene; 23S RNA gene; ds.
XX
OS   Escherichia coli.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    complement (1..121)
FT                   /*tag=  a
FT                   /label= 5S
FT   misc_feature    complement (449..3362)
FT                   /*tag=  b
FT                   /label= 23S
FT   misc_feature    complement (3800..5341)
FT                   /*tag=  c
FT                   /label= 16S
XX
PN   WO9905325-A1.
XX
PD   04-FEB-1999.
XX
PF   24-JUL-1998;   98WO-US15464.
XX
PR   25-JUL-1997;   97US-0053097.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Goldstein RN;
XX
DR   WPI; 1999-142969/12.
XX
PT   Determining species of bacteria and fungi - useful for
PT   distinguishing between bacterial/fungal species, and for determining
PT   the identity of bacterial/fungal pathogens in biological samples
XX
PS   Disclosure; Fig 7 (39/67-42/67); 133pp; English.
XX
CC   This is the DNA sequence of the Escherichia coli strain MG1655
CC   rrnD operon (16S-spacer-23S-spacer-5S).  Restriction sites for
CC   enzymes cutting the operon 5 times or less have been determined.
CC   E. coli rrnA-rrnH operon sequences are provided (see AAX24983-89).
CC   Methods and compositions are described for determining the species
CC   of an unknown bacterium or fungus in a sample.  The method involves
CC   isolating and digesting bacterial (or fungal) DNA encoding 16S and
CC   23S rRNA from a sample with restriction enzymes, detecting the
CC   products, and comparing them to signature bands from a number of
CC   bacteria.  The method generates a species-conserved set of RFLP
CC   bands, unique for each species.  These species-conserved sets
CC   represent precise markers appopropriate for inter-species
CC   discriminatory purposes (i.e. to determine the species of a given,
CC   unknown isolate e.g. in a clinical specimen).  In contrast to
CC   conventional ribotyping, the present invention utilises the
CC   ribosomal operon sequences which vary less than 3% (and more
CC   preferably less than 2%) within a species and vary between species.
CC   The method is useful for medical, food, agricultural and
CC   environmental testing.  It does not require sequencing of nucleic
CC   acid from biological samples.
XX
SQ   Sequence 5341 BP; 1117 A; 1647 C; 1188 G; 1389 T; 0 other;

  Query Match             90.6%;  Score 15.4;  DB 20;  Length 5341;
  Best Local Similarity   94.1%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db   1295 cggggtctttccgtctt 1311


RESULT  29
AAA81793/c
ID   AAA81793 standard; DNA; 435 BP.
XX
AC   AAA81793;
XX
DT   04-DEC-2000  (first entry)
XX
DE   N. meningitidis partial DNA sequence gnm_340 SEQ ID NO:340.
XX
KW   Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic;
KW   antigen; vaccine; diagnosis; infection; antibacterial; identification;
KW   Meningococcus B; MenB; ds.
XX
OS   Neisseria meningitidis.
XX
PN   WO200022430-A2.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-US23573.
XX
PR   09-OCT-1998;   98US-0103794.
PR   30-APR-1999;   99US-0132068.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Frazer CM,  Hickey E,  Peterson J,  Tettelin H,  Venter JC;
```

PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
PI Rappuoli R, Pizza M;
XX
DR WPI; 2000-318079/27.
XX
PT Isolated nucleotide sequences of Neisseria meningitidis which can be
PT used in the diagnosis and treatment of N. meningitidis infection and
PT other Neisserial infections, for example, N.gonorrhoea -
XX
PS Claim 7; Page 1599; 1760pp; English.
XX
CC The present invention describes methods of obtaining immunogenic
CC proteins from Neisseria genomic sequences. AAA81453 to AAA82414
CC represent specifically claimed Neisseria meningitidis genomic DNA
CC sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
CC Neisseria DNA sequences and their corresponding proteins; AAA81254 to
CC AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
CC isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
CC AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
CC sequences, which are all used in the exemplification of the present
CC invention. The nucleic acid sequences, protein sequences, and antibodies
CC against them, can be used in the manufacture of a composition. The
CC composition can be used as a medicament (or in the manufacture of a
CC medicament) for treating, preventing or diagnosing infection due to
CC Neisserial bacteria. For example, some of the identified proteins could
CC be components of vaccines against Meningococcus B; against all serotypes;
CC and/or against all pathogenic Neissariae. Identification of sequences
CC from the bacterium will also facilitate production of biological probes,
CC particularly organism-specific probes. Attempts to make efficacious
CC Meningococcus B vaccines have failed mainly due to antigen tolerance.
CC Multivalent vaccines have also been tried but none have successfully
CC overcome antigenic variability. The provision of further, complete
CC sequences may provide an opportunity to identify secreted or surface
CC exposed proteins that may be presumed targets for the immune system and
CC which are not antigenically variable or at least more conserved than
CC other more variable regions.
XX
SQ Sequence 435 BP; 103 A; 108 C; 123 G; 101 T; 0 other;

Query Match 84.7%; Score 14.4; DB 21; Length 435;
Best Local Similarity 93.8%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtct 16
||||||||| ||||||
Db 227 CGGGGTCTTGCCGTCT 212

RESULT 30
AAI91211/c
ID AAI91211 standard; cDNA; 473 BP.
XX
AC AAI91211;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 11271.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR P-PSDB; AA011280.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 1; SEQ ID NO 11271; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 473 BP; 151 A; 117 C; 115 G; 81 T; 9 other;

Query Match 84.7%; Score 14.4; DB 22; Length 473;
Best Local Similarity 93.8%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ggggtcttcccgtctt 17
||||| ||||||||||
Db 172 GGGGTTTTCCCGTCTT 157

RESULT 31
AAX21151/c
ID AAX21151 standard; DNA; 509 BP.
XX
AC AAX21151;
XX
DT 05-MAY-1999 (first entry)
XX
DE Polynucleotide sequence from the genome of Treponema pallidum.
XX
KW Treponema pallidum infection; syphilis; Borrelia infection; animal;
KW enzyme production; ds.
XX
OS Treponema pallidum.
XX
PN WO9859034-A2.
XX
PD 30-DEC-1998.
XX
PF 23-JUN-1998; 98WO-US13041.
XX
PR 24-JUN-1997; 97US-0050667.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Fraser CM;
XX
DR WPI; 1999-081273/07.
XX
PT New isolated Treponema pallidum nucleic acids - used to develop
PT products for the detection, diagnosis, characterisation, prevention

PT and therapy of T. pallidum infections, particularly syphilis
XX
PS Claim 1; Page 1094; 1150pp; English.
XX
CC AAX20500-21243 represent polynucleotide sequences from the genome of
CC Treponema pallidum. The sequences can be used for detection,
CC diagnosis, characterisation, prevention and therapy for T. pallidum
CC infections, particularly syphilis. They can also be used for detecting
CC diseases related to Borrelia infections in animals, and for the
CC production of biosynthetic products such as enzymes.
XX
SQ Sequence 509 BP; 134 A; 111 C; 149 G; 113 T; 2 other;

Query Match 84.7%; Score 14.4; DB 20; Length 509;
Best Local Similarity 93.8%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtct 16
||||||||| ||||||
Db 287 CGGGGTCTTTCCGTCT 272

RESULT 32
AAA81810
ID AAA81810 standard; DNA; 597 BP.
XX
AC AAA81810;
XX
DT 04-DEC-2000 (first entry)
XX
DE N. meningitidis partial DNA sequence gnm_357 SEQ ID NO:357.
XX
KW Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic;
KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
KW Meningococcus B; MenB; ds.
XX
OS Neisseria meningitidis.
XX
PN WO200022430-A2.
XX
PD 20-APR-2000.
XX
PF 08-OCT-1999; 99WO-US23573.
XX
PR 09-OCT-1998; 98US-0103794.
PR 30-APR-1999; 99US-0132068.
XX
PA (CHIR) CHIRON CORP.
XX
PI Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;
PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
PI Rappuoli R, Pizza M;
XX
DR WPI; 2000-318079/27.
XX
PT Isolated nucleotide sequences of a meningitidis which can be
PT used in the diagnosis and treatme meningitidis infection and
PT other Neisserial infections, for N.gonorrhoea -
XX
PS Claim 7; Page 1604; 1760pp; Engl
XX
CC The present invention describes methods of obtaining immunogenic
CC proteins from Neisseria genomic sequences. AAA81453 to AAA82414
CC represent specifically claimed Neisseria meningitidis genomic DNA
CC sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
CC Neisseria DNA sequences and their corresponding proteins; AAA81254 to
CC AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
CC isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
CC AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
CC sequences, which are all used in the exemplification of the present
CC invention. The nucleic acid sequences, protein sequences, and antibodies
CC against them, can be used in the manufacture of a composition. The
CC composition can be used as a medicament (or in the manufacture of a
CC medicament) for treating, preventing or diagnosing infection due to
CC Neisserial bacteria. For example, some of the identified proteins could
CC be components of vaccines against Meningococcus B; against all serotypes;
CC and/or against all pathogenic Neissariae. Identification of sequences
CC from the bacterium will also facilitate production of biological probes,
CC particularly organism-specific probes. Attempts to make efficacious
CC Meningococcus B vaccines have failed mainly due to antigen tolerance.
CC Multivalent vaccines have also been tried but none have successfully
CC overcome antigenic variability. The provision of further, complete
CC sequences may provide an opportunity to identify secreted or surface
CC exposed proteins that may be presumed targets for the immune system and
CC which are not antigenically variable or at least more conserved than
CC other more variable regions.
XX
SQ Sequence 597 BP; 132 A; 183 C; 137 G; 145 T; 0 other;

Query Match 84.7%; Score 14.4; DB 21; Length 597;
Best Local Similarity 93.8%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtct 16
||||||||| ||||||
Db 374 cggggtctttccgtct 389

RESULT 33
AAF12552/c
ID AAF12552 standard; cDNA; 650 BP.
XX
AC AAF12552;
XX
DT 13-MAR-2001 (first entry)
XX
DE Aspergillus oryzae EST SEQ ID NO:5075.
XX
KW Multiple gene expression; filamentous fungal cell; EST;
KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;
KW culture condition; environmental stress; spore morphogenesis;
KW metabolic pathway engineering; catabolic pathway engineering; ss.
XX
OS Aspergillus oryzae.
XX
PN WO200056762-A2.
XX
PD 28-SEP-2000.
XX
PF 22-MAR-2000; 2000WO-US07781.
XX
PR 22-MAR-1999; 99US-0273623.
XX
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO NORDISK AS.
XX
PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
XX
DR WPI; 2000-594572/56.
XX
PT Monitoring differential expression of genes in filamentous fungal cells
PT uses fluorescence-labeled nucleic acids isolated from the cells and a
PT substrate of expressed sequence tags -
XX
PS Claim 88; Page 2129; 3161pp; English.
XX
CC The present invention describes a method for monitoring differential
CC expression of genes in a first filamentous fungal (FF) cell relative to
CC expression of the same genes in one or more second filamentous fungal
CC cells. The method uses fluorescence-labeled nucleic acids isolated from
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
CC are used in the methods for monitoring differential expression of genes
CC in a first filamentous fungal (FF) cell relative to expression of the

CC same genes in one or more second filamentous fungal cells. Monitoring
CC the global expression of genes from FF cells allows the production
CC potential of the microorganisms to be improved. New genes may be
CC discovered, possible functions of unknown open reading frames can be
CC identified and gene copy number variation and stability can be
CC monitored. The expression of genes can be used to study how FF cells
CC adapt to changes in culture conditions, environmental stress, spore
CC morphogenesis, recombination, metabolic or catabolic pathway
CC engineering. Using ESTs provides several advantages over genomic or
CC random cDNA clones including elimination of redundancy as one spot on an
CC array equals one gene or open reading frame, and organisation of the
CC microarrays based on function of the gene products to facilitate
CC analysis of the results. AAF07478 to AAF11247 represents ESTs from
CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
CC all specifically claimed in the present invention.
XX
SQ Sequence 650 BP; 186 A; 163 C; 157 G; 144 T; 0 other;

Query Match 84.7%; Score 14.4; DB 21; Length 650;
Best Local Similarity 93.8%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ggggtcttcccgtctt 17
||| ||||||||||||
Db 369 GGGCTCTTCCCGTCTT 354

RESULT 34
AAC43891/c
ID AAC43891 standard; DNA; 741 BP.
XX
AC AAC43891;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 40884.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.

PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 84.7%; Score 14.4; DB 21; Length 741;
Best Local Similarity 93.8%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 cggggtcttcccgtct 16
          ||||||||| ||||||
Db    274 CGGGGTCTTACCGTCT 259
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RESULT 35
AAS54060/c
ID AAS54060 standard; DNA; 1065 BP.
XX
AC AAS54060;
XX
DT 13-FEB-2002 (first entry)
XX
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #191.
XX
KW Antisense; ds; prokaryotic cellular proliferation gene;
KW antibiotic; antibacterial; drug design.
XX
OS Pseudomonas aeruginosa.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR P-PSDB; AAU36201.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
PS Claim 27; Seq ID No 7697; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used

CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence encodes an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1065 BP; 216 A; 370 C; 315 G; 164 T; 0 other;

Query Match 84.7%; Score 14.4; DB 23; Length 1065;
Best Local Similarity 93.8%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ggggtcttcccgtctt 17
||||||||| |||||||
Db 344 GGGGTCTTGCCGTCTT 329

RESULT 36
AAC60039/c
ID AAC60039 standard; cDNA; 1430 BP.
XX
AC AAC60039;
XX
DT 26-JAN-2001 (first entry)
XX
DE Human secreted protein gene 15 SEQ ID NO:25.
XX
KW Human; secreted protein; neuroprotective; cytostatic; cardioactive;
KW immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic;
KW antiinfective; gynaecological; antibacterial; neural disorder; cancer;
KW immune disease; reproductive disorder; proliferative disorder;
KW gastrointestinal disease; wound healing; infectious disease;
KW food additive; ss.
XX
OS Homo sapiens.
XX
PN WO200056766-A1.
XX
PD 28-SEP-2000.
XX
PF 16-MAR-2000; 2000WO-US06824.
XX
PR 19-MAR-1999; 99US-0125359.
PR 03-DEC-1999; 99US-0168664.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-594574/56.
DR P-PSDB; AAB34868.
XX
PT Human secreted proteins and gene sequences encoding them, useful for
PT detection, prevention, and treatment of various disorders such as
PT cancer and immune system disorders -
XX
PS Claim 1; Page 359; 442pp; English.
XX
CC The polynucleotide sequences given in AAC60025-C60071 encode the human
CC secreted proteins represented in AAB34854-B34900. Sequences
CC AAB34901-B34976 are fragments of proteins encoded by the genes, and also
CC proteins with which they share sequence homology. The proteins have
CC activities based on the tissues in which their encoding genes are
CC expressed. Examples of the proteins activities include: neuroprotective;
CC cytostatic; cardioactive; immunomodulatory; general muscular activity;
CC vulnerary; general gastrointestinal activity; nephrotropic;
CC antiinfective; gynaecological; and antibacterial. The human secreted
CC proteins, polynucleotides, antagonists and antagonists of the invention
CC may be useful in treating, preventing and/or diagnosing various
CC diseases, disorders and conditions such as neural, immune, muscular,
CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal and
CC proliferative disorders and cancer. They may also be used in the
CC treatment of wounds, and infectious diseases. The polypeptides may be
CC used as a food additive or preservative to increase storage capabilities.
CC Sequences AAC60016-C60024 and AAB34853 are used in the course of the
CC invention during the identification and characterisation of the protein
CC and nucleotide sequences.
XX
SQ Sequence 1430 BP; 350 A; 365 C; 406 G; 309 T; 0 other;

Query Match 84.7%; Score 14.4; DB 21; Length 1430;
Best Local Similarity 93.8%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ggggtcttcccgtctt 17
||||||||||| ||||
Db 316 GGGGTCTTCCCATCTT 301

RESULT 37
AAH90047/c
ID AAH90047 standard; cDNA; 1442 BP.
XX
AC AAH90047;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human bone marrow cDNA, SEQ ID NO: 291.
XX
KW Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;
KW antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
KW immunosuppressive; gene therapy; cytokine cell proliferation;
KW cell differentiation modulator; immune disorder; infection; cancer;
KW human immunodeficiency virus; HIV; autoimmune disorder; haemophilia; ss.
XX
OS Homo sapiens.
XX
PN WO200153453-A2.
XX
PD 26-JUL-2001.
XX
PF 23-DEC-2000; 2000WO-US34960.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 30-NOV-2000; 2000US-0250583.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y;
PI Ren F, Wang J, Werhman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Drmanac RT;
XX
DR WPI; 2001-488707/53.
DR P-PSDB; AAM00928.
XX
PT Novel bone-marrow-expressed polynucleotides and polypeptides, useful
PT for treating e.g. cancer and immune deficiency disorders -
XX
PS Claim 1; Page 403; 648pp; English.
XX
CC The present sequence is one of 251 novel human polynucleotides
CC expressed in the bone marrow. The polynucleotide and the

```
CC   polypeptide encoded by it are useful in the treatment of various
CC   immune deficiencies and disorders. The deficiencies and disorders may
CC   be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal
CC   infection, or may result from an autoimmune disorder, a coagulation
CC   disorder (e.g. haemophilia), inhibition of tumour cell proliferation,
CC   suppression of an inflammatory response or treatment of a nervous
CC   system disorder such as Alzheimer's disease. Detection of the presence
CC   or increased expression of the polynucleotide or the protein it
CC   encodes is useful for the diagnosis and/or prognosis of one
CC   or more types of cancer. The polynucleotide and polypeptide can be
CC   used as nutritional sources or supplements and in the screening of
CC   chemical compounds as potential drugs.
XX
SQ   Sequence 1442 BP; 428 A; 375 C; 335 G; 304 T; 0 other;


  Query Match             84.7%;  Score 14.4;  DB 22;  Length 1442;
  Best Local Similarity   93.8%;  Pred. No. 4.3e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ggggtcttcccgtctt 17
           |||||||||| |||||
Db     910 GGGGTCTTCCTGTCTT 895


RESULT  38
AAH90100/c
ID   AAH90100 standard; cDNA; 1593 BP.
XX
AC   AAH90100;
XX
DT   01-OCT-2001  (first entry)
XX
DE   Human bone marrow cDNA, SEQ ID NO: 457.
XX
KW   Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;
KW   antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
KW   immunosuppressive; gene therapy; cytokine cell proliferation;
KW   cell differentiation modulator; immune disorder; infection; cancer;
KW   human immunodeficiency virus; HIV; autoimmune disorder; haemophilia; ss.
XX
OS   Homo sapiens.
XX
PN   WO200153453-A2.
XX
PD   26-JUL-2001.
XX
PF   23-DEC-2000; 2000WO-US34960.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
PR   09-JUL-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   03-AUG-2000; 2000US-0653450.
PR   14-SEP-2000; 2000US-0662191.
PR   19-OCT-2000; 2000US-0693036.
PR   30-NOV-2000; 2000US-0250583.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Ford JE,  Boyle BJ,  Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y;
PI   Ren F,  Wang J,  Werhman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J;
PI   Zhao QA,  Zhou P,  Drmanac RT;
XX
DR   WPI; 2001-488707/53.
DR   P-PSDB; AAM00981.
XX
PT   Novel bone-marrow-expressed polynucleotides and polypeptides, useful
PT   for treating e.g. cancer and immune deficiency disorders -
XX
PS   Claim 1; Page 544-545; 648pp; English.
XX
CC   The present sequence is one of 251 novel human polynucleotides
CC   expressed in the bone marrow. The polynucleotide and the
CC   polypeptide encoded by it are useful in the treatment of various
CC   immune deficiencies and disorders. The deficiencies and disorders may
CC   be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal
CC   infection, or may result from an autoimmune disorder, a coagulation
CC   disorder (e.g. haemophilia), inhibition of tumour cell proliferation,
CC   suppression of an inflammatory response or treatment of a nervous
CC   system disorder such as Alzheimer's disease. Detection of the presence
CC   or increased expression of the polynucleotide or the protein it
CC   encodes is useful for the diagnosis and/or prognosis of one
CC   or more types of cancer. The polynucleotide and polypeptide can be
CC   used as nutritional sources or supplements and in the screening of
CC   chemical compounds as potential drugs.
XX
SQ   Sequence 1593 BP; 465 A; 414 C; 380 G; 334 T; 0 other;


  Query Match             84.7%;  Score 14.4;  DB 22;  Length 1593;
  Best Local Similarity   93.8%;  Pred. No. 4.3e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ggggtcttcccgtctt 17
           |||||||||| |||||
Db    1061 GGGGTCTTCCTGTCTT 1046


RESULT  39
AAX22111/c
ID   AAX22111 standard; DNA; 1725 BP.
XX
AC   AAX22111;
XX
DT   18-MAY-1999  (first entry)
XX
DE   Human secreted protein gene 1 clone HTXBK30.
XX
KW   Human; secreted protein; gene therapy; protein therapy; tissue; cancer;
KW   tumour; neurodegenerative disorder; leukaemia; autoimmune disease; AIDS;
KW   developmental abnormality; foetal deficiency; Alzheimer's disease;
KW   cognitive disorder; schizophrenia; immunological disorder; mood disorder;
KW   immune deficiency disease; respiratory disorder; arthritis; skeletal;
KW   haematopoietic disorder; neural; osteoporosis; metabolic disorders;
KW   cardiovascular; endocrine; gastrointestinal; asthma; diagnosis; ds.
XX
OS   Homo sapiens.
XX
PN   WO9901020-A2.
XX
PD   14-JAN-1999.
XX
PF   30-JUN-1998;   98WO-US13608.
XX
PR   12-SEP-1997;   97US-0058663.
PR   01-JUL-1997;   97US-0051381.
PR   01-JUL-1997;   97US-0051480.
PR   12-SEP-1997;   97US-0058598.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Carter KC,  Endress GA,  Feng P,  Rosen CA,  Ruben SM;
XX
DR   WPI; 1999-105683/09.
DR   P-PSDB; AAY01135, AAY01159, AAY01160, AAY01161.
XX
PT   New isolated human genes and the secreted polypeptides they encode -
PT   useful for diagnosis and treatment of e.g. cancers, neurological
PT   disorders, immune diseases, immune deficiency diseases or blood
PT   disorders
XX
PS   Claim 4; Page 115-116; 179pp; English.
XX
CC   The invention relates to nucleic acid sequences (AAX22111 to AAX22134)
CC   encoding human secreted proteins (AAY01135 to AAY01158). The secreted
```

CC protein gene sequences are deposited with the ATCC under deposit number
CC ATCC 209118. Host cells comprising recombinant vectors containing the
CC nucleic acid sequences are used for the recombinant production of the
CC secreted proteins. The polynucleotide and amino acid sequences are useful
CC for are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Pathological conditions can
CC be also diagnosed by determining the amount of the new polypeptides in a
CC sample or by determining the presence of mutations in the new
CC polynucleotides. Specific uses are described for each of the
CC polynucleotides, based on which tissues they are most highly expressed
CC in, and include developing products for the diagnosis or treatment of
CC cancer, tumours, developmental abnormalities and foetal deficiencies,
CC autoimmune diseases, lymphomas, Alzheimer's and cognitive disorders,
CC schizophrenia, immunological disorders, immune deficiency diseases
CC (AIDS), mood disorders, respiratory disorders, arthritis, asthma,
CC haematopoietic disorders, neural disorders, skeletal disorders,
CC osteoporosis, metabolic disorders, cardiovascular disorders, endocrine
CC disorders or gastrointestinal disorders. The polypeptides are also useful
CC for identifying their binding partners. The present sequence represents a
CC gene encoding a human secreted protein (see descriptor line for gene
CC number and clone identification).
XX
SQ Sequence 1725 BP; 449 A; 514 C; 415 G; 339 T; 8 other;

Query Match 84.7%; Score 14.4; DB 20; Length 1725;
Best Local Similarity 93.8%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ggggtcttcccgtctt 17
||||||||||| |||||
Db 223 GGGGTCTTCCTGTCTT 208

RESULT 40
ABL11755
ID ABL11755 standard; cDNA; 1902 BP.
XX
AC ABL11755;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29747.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB67652.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 29747; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1902 BP; 485 A; 434 C; 456 G; 527 T; 0 other;

Query Match 84.7%; Score 14.4; DB 23; Length 1902;
Best Local Similarity 93.8%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtct 16
|| ||||||||||||||
Db 1702 cgaggtcttcccgtct 1717

RESULT 41
AAV72295/c
ID AAV72295 standard; DNA; 2061 BP.
XX
AC AAV72295;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human blood bacterium 23S rRNA DNA #2.
XX
KW 16S rRNA; drug resistant protein; pathophysiology; human blood bacterium;
KW disease; multiple sclerosis; chronic fatigue; treatment; fibromyalgia;
KW lupus erythematosis; rheumatoid arthritis; toxic metabolite; plasma;
KW serum; antibiotic; vaccine; antibiotic; 23S rRNA; ss.
XX
OS Bacteria.
XX
PN WO9924613-A1.
XX
PD 20-MAY-1999.
XX
PF 06-NOV-1998; 98WO-US23674.
XX
PR 06-NOV-1997; 97US-0064472.
XX
PA (PATH-) PATHOBIOTEK INC.
XX
PI Lindner L, MacPhee K;
XX
DR WPI; 1999-327419/27.
XX
PT A human blood bacterium, characterization, culturing and diagnostic
PT methods
XX
PS Claim 26; Page 86-87; 95pp; English.
XX
CC This invention describes methods for culturing and detecting a human
CC blood bacterium (HBB), implicated in several disease e.g. multiple
CC sclerosis and chronic fatigue. Quantification of levels of HBB in an
CC individual can be used to determine the efficacy of a treatment for a
CC HBB-related disease. HBB-related diseases include chronic fatigue
CC syndrome, multiple sclerosis, lupus erythematosis, rheumatoid arthritis
CC and fibromyalgia. HBB vaccines can be used to treat diseased individuals.
CC Engineered HBB is administered to individuals where the disease has the
CC condition of a toxic metabolite being accumulated in plasma or serum of
CC the individual. A range of antibiotics can be used to treat
CC pathophysiological states associated with HBB. The invention describes
CC the isolation of HBB 16S rRNA, 23S rRNA and drug resistant protein
CC encoding nucleic acid. The products of the invention have antibiotic
CC activity.
XX

```
SQ   Sequence 2061 BP; 507 A; 511 C; 659 G; 384 T; 0 other;

  Query Match             84.7%;  Score 14.4;  DB 20;  Length 2061;
  Best Local Similarity   93.8%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtct 16
           ||||||||| ||||||
Db    1865 CGGGGTCTTTCCGTCT 1850


RESULT  42
AAH89934/c
ID   AAH89934 standard; cDNA; 2222 BP.
XX
AC   AAH89934;
XX
DT   01-OCT-2001  (first entry)
XX
DE   Human bone marrow cDNA, SEQ ID NO: 65.
XX
KW   Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;
KW   antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
KW   immunosuppressive; gene therapy; cytokine cell proliferation;
KW   cell differentiation modulator; immune disorder; infection; cancer;
KW   human immunodeficiency virus; HIV; autoimmune disorder; haemophilia; ss.
XX
OS   Homo sapiens.
XX
PN   WO200153453-A2.
XX
PD   26-JUL-2001.
XX
PF   23-DEC-2000; 2000WO-US34960.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
PR   09-JUL-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   03-AUG-2000; 2000US-0653450.
PR   14-SEP-2000; 2000US-0662191.
PR   19-OCT-2000; 2000US-0693036.
PR   30-NOV-2000; 2000US-0250583.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Ford JE,  Boyle BJ,  Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y;
PI   Ren F,  Wang J,  Werhman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J;
PI   Zhao QA,  Zhou P,  Drmanac RT;
XX
DR   WPI; 2001-488707/53.
DR   P-PSDB; AAM00815.
XX
PT   Novel bone-marrow-expressed polynucleotides and polypeptides, useful
PT   for treating e.g. cancer and immune deficiency disorders -
XX
PS   Claim 1; Page 250-251; 648pp; English.
XX
CC   The present sequence is one of 251 novel human polynucleotides
CC   expressed in the bone marrow. The polynucleotide and the
CC   polypeptide encoded by it are useful in the treatment of various
CC   immune deficiencies and disorders. The deficiencies and disorders may
CC   be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal
CC   infection, or may result from an autoimmune disorder, a coagulation
CC   disorder (e.g. haemophilia), inhibition of tumour cell proliferation,
CC   suppression of an inflammatory response or treatment of a nervous
CC   system disorder such as Alzheimer's disease. Detection of the presence
CC   or increased expression of the polynucleotide or the protein it
CC   encodes is useful for the diagnosis and/or prognosis of one
CC   or more types of cancer. The polynucleotide and polypeptide can be
CC   used as nutritional sources or supplements and in the screening of
CC   chemical compounds as potential drugs.
XX
SQ   Sequence 2222 BP; 619 A; 643 C; 526 G; 433 T; 1 other;

  Query Match             84.7%;  Score 14.4;  DB 22;  Length 2222;
  Best Local Similarity   93.8%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ggggtcttcccgtctt 17
           |||||||||| |||||
Db     910 GGGGTCTTCCTGTCTT 895


RESULT  43
AAV72294/c
ID   AAV72294 standard; DNA; 2542 BP.
XX
AC   AAV72294;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human blood bacterium 23S rRNA DNA #1.
XX
KW   16S rRNA; drug resistant protein; pathophysiology; human blood bacterium;
KW   disease; multiple sclerosis; chronic fatigue; treatment; fibromyalgia;
KW   lupus erythematosis; rheumatoid arthritis; toxic metabolite; plasma;
KW   serum; antibiotic; vaccine; antibiotic; 23S rRNA; ss.
XX
OS   Bacteria.
XX
PN   WO9924613-A1.
XX
PD   20-MAY-1999.
XX
PF   06-NOV-1998;  98WO-US23674.
XX
PR   06-NOV-1997;  97US-0064472.
XX
PA   (PATH-) PATHOBIOTEK INC.
XX
PI   Lindner L,  MacPhee K;
XX
DR   WPI; 1999-327419/27.
XX
PT   A human blood bacterium, characterization, culturing and diagnostic
PT   methods
XX
PS   Claim 25; Page 85-86; 95pp; English.
XX
CC   This invention describes methods for culturing and detecting a human
CC   blood bacterium (HBB), implicated in several disease e.g. multiple
CC   sclerosis and chronic fatigue. Quantification of levels of HBB in an
CC   individual can be used to determine the efficacy of a treatment for a
CC   HBB-related disease. HBB-related diseases include chronic fatigue
CC   syndrome, multiple sclerosis, lupus erythematosis, rheumatoid arthritis
CC   and fibromyalgia. HBB vaccines can be used to treat diseased individuals.
CC   Engineered HBB is administered to individuals where the disease has the
CC   condition of a toxic metabolite being accumulated in plasma or serum of
CC   the individual. A range of antibiotics can be used to treat
CC   pathophysiological states associated with HBB. The invention describes
CC   the isolation of HBB 16S rRNA, 23S rRNA and drug resistant protein
CC   encoding nucleic acid. The products of the invention have antibiotic
CC   activity.
XX
SQ   Sequence 2542 BP; 615 A; 623 C; 833 G; 471 T; 0 other;

  Query Match             84.7%;  Score 14.4;  DB 20;  Length 2542;
  Best Local Similarity   93.8%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtct 16
           ||||||||| ||||||
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Db   1867 CGGGGTCTTTCCGTCT 1852


RESULT  44
AAC76013/c
ID   AAC76013 standard; cDNA; 3166 BP.
XX
AC   AAC76013;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human ORFX ORF1568 polynucleotide sequence SEQ ID NO:3135.
XX
KW   Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW   vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW   anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW   immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW   hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW   antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW   antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW   neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW   cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW   cholesterol ester storage; systemic lupus erythematosus; infection;
KW   severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW   allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW   bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW   thrombosis; contraceptive; ss.
XX
OS   Homo sapiens.
XX
PN   WO200058473-A2.
XX
PD   05-OCT-2000.
XX
PF   31-MAR-2000; 2000WO-US08621.
XX
PR   31-MAR-1999;   99US-0127607.
PR   02-APR-1999;   99US-0127636.
PR   05-APR-1999;   99US-0127728.
PR   30-MAR-2000; 2000US-0540763.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2000-602362/57.
DR   P-PSDB; AAB41804.
XX
PT   Novel nucleic acids and peptides derived from open reading frame X,
PT   useful for treating e.g. cancers, proliferative disorders,
PT   neurodegenerative disorders and cardiovascular disease -
XX
PS   Claim 5; Page 2351-2353; 5507pp; English.
XX
CC   AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC   which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC   sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC   antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
CC   osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC   immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC   antidiabetic; hypotensive; dermatological; immunosuppressive;
CC   antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC   antithyroid; and antianaemic. The sequences can be used for determining
CC   the presence of or predisposition to, or preventing or treating
CC   pathological conditions associated with an ORFX-associated disorder. The
CC   nucleic acids can be used to express ORFX proteins in gene therapy
CC   vectors. The proteins and nucleic acids may be used to treat cancers,
CC   proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC   graft vs host disease, cardiovascular disease, diabetes mellitus,
CC   hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC   erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC   bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC   allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC   nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC   coagulation; to inhibit thrombosis; and as a contraceptive.
XX
SQ   Sequence 3166 BP; 862 A; 761 C; 726 G; 815 T; 2 other;


  Query Match             84.7%;  Score 14.4;  DB 21;  Length 3166;
  Best Local Similarity   93.8%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ggggtcttcccgtctt 17
           ||||||||||| |||||
Db     182 GGGGTCTTCCTGTCTT 167


RESULT  45
AAX20282/c
ID   AAX20282 standard; DNA; 3398 BP.
XX
AC   AAX20282;
XX
DT   04-MAY-1999  (first entry)
XX
DE   Borrelia burgdorferi polynucleotide sequence #35.
XX
KW   Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;
KW   epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;
KW   infection; diagnosis; characterisation; detection; ds.
XX
OS   Borrelia burgdorferi.
XX
PN   WO9858943-A1.
XX
PD   30-DEC-1998.
XX
PF   18-JUN-1998;   98WO-US12764.
XX
PR   03-SEP-1997;   97US-0057483.
PR   20-JUN-1997;   97US-0050359.
PR   22-JUL-1997;   97US-0053344.
PR   22-JUL-1997;   97US-0053377.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (MEDI-) MEDIMMUNE INC.
XX
PI   Clayton R,  Dougherty BA,  Fraser C,  Lathigra R,  Smith HO;
PI   White OR;
XX
DR   WPI; 1999-081217/07.
XX
PT   New isolated Borrelia burgdorferi nucleic acids - used to develop
PT   products for the detection, diagnosis, characterisation, prevention
PT   and therapy of infections, particularly Lyme disease
XX
PS   Claim 1; Page 998-1000; 1128pp; English.
XX
CC   AAX20248 to AAX20402 represent polynucleotide sequences isolated from
CC   Borrelia burgdorferi (Bb). Products derived from Bb can be used for
CC   the detection, diagnosis, characterisation, prevention and therapy of
CC   Bb infections, e.g. Lyme disease. They can also be used for the
CC   production of biosynthetic products, e.g. enzymes. Borrelia belongs
CC   to a family of motile, spiral-shaped bacteria called Spirochetes.
CC   Spirochetes are pathogenic in humans and Borrelia causes epidemic and
CC   endemic relapsing fever, and Lyme borreliosis, more commonly known as
CC   Lyme disease.
XX
SQ   Sequence 3398 BP; 1096 A; 535 C; 869 G; 896 T; 2 other;


  Query Match             84.7%;  Score 14.4;  DB 20;  Length 3398;
  Best Local Similarity   93.8%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy      1 cggggtcttcccgtct 16
          ||||||||| ||||||
Db   2497 CGGGGTCTTTCCGTCT 2482


RESULT  46
AAX24982/c
ID   AAX24982 standard; DNA; 5273 BP.
XX
AC   AAX24982;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Haemophilus influenzae Rd rrnB operon (16S-spacer-23S-spacer-5S).
XX
KW   Speciation; ribotyping; species discrimination; marker; RFLP;
KW   restriction fragment length polymorphism; bacterium; fungus;
KW   pathogen; rrnB operon; 16S RNA gene; 23S RNA gene; ds.
XX
OS   Haemophilus influenzae.
XX
PN   WO9905325-A1.
XX
PD   04-FEB-1999.
XX
PF   24-JUL-1998;   98WO-US15464.
XX
PR   25-JUL-1997;   97US-0053097.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Goldstein RN;
XX
DR   WPI; 1999-142969/12.
XX
PT   Determining species of bacteria and fungi - useful for
PT   distinguishing between bacterial/fungal species, and for determining
PT   the identity of bacterial/fungal pathogens in biological samples
XX
PS   Disclosure; Fig 4(10/67-15/67); 133pp; English.
XX
CC   This is the DNA sequence of the Haemophilus influenzae strain Rd
CC   rrnB operon (16S-spacer-23S-spacer-5S).  Restriction sites for
CC   enzymes cutting the operon 5 times or less have been determined.
CC   The H. influenzae Rd rrnA operon is also provided (see AAX24981).
CC   Methods and compositions are described for determining the species
CC   of an unknown bacterium or fungus in a sample.  The method involves
CC   isolating and digesting bacterial (or fungal) DNA encoding 16S and
CC   23S rRNA from a sample with restriction enzymes, detecting the
CC   products, and comparing them to signature bands from a number of
CC   bacteria.  The method generates a species-conserved set of RFLP
CC   bands, unique for each species.  These species-conserved sets
CC   represent precise markers appopropriate for inter-species
CC   discriminatory purposes (i.e. to determine the species of a given,
CC   unknown isolate e.g. in a clinical specimen).  In contrast to
CC   conventional ribotyping, the present invention utilises the
CC   ribosomal operon sequences which vary less than 3% (and more
CC   preferably less than 2%) within a species and vary between species.
CC   The method is useful for medical, food, agricultural and
CC   environmental testing.  It does not require sequencing of nucleic
CC   acid from biological samples.
XX
SQ   Sequence 5273 BP; 1565 A; 1014 C; 1557 G; 1137 T; 0 other;

  Query Match             84.7%;  Score 14.4;  DB 20;  Length 5273;
  Best Local Similarity   93.8%;  Pred. No. 4.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtct 16
          ||||||||| ||||||
Db   4082 CGGGGTCTTTCCGTCT 4067


RESULT  47
AAX24981/c
ID   AAX24981 standard; DNA; 5519 BP.
XX
AC   AAX24981;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Haemophilus influenzae Rd rrnA operon (16S-spacer-23S-spacer-5S).
XX
KW   Speciation; ribotyping; species discrimination; marker; RFLP;
KW   restriction fragment length polymorphism; bacterium; fungus;
KW   pathogen; rrnA operon; 16S RNA gene; 23S RNA gene; ds.
XX
OS   Haemophilus influenzae.
XX
PN   WO9905325-A1.
XX
PD   04-FEB-1999.
XX
PF   24-JUL-1998;   98WO-US15464.
XX
PR   25-JUL-1997;   97US-0053097.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Goldstein RN;
XX
DR   WPI; 1999-142969/12.
XX
PT   Determining species of bacteria and fungi - useful for
PT   distinguishing between bacterial/fungal species, and for determining
PT   the identity of bacterial/fungal pathogens in biological samples
XX
PS   Disclosure; Fig 4 (4/67-9/67); 133pp; English.
XX
CC   This is the DNA sequence of the Haemophilus influenzae strain Rd
CC   rrnA operon (16S-spacer-23S-spacer-5S).  Restriction sites for
CC   enzymes cutting the operon 5 times or less have been determined.
CC   The H. influenzae Rd rrnB operon is also provided (see AAX24982).
CC   Methods and compositions are described for determining the species
CC   of an unknown bacterium or fungus in a sample.  The method involves
CC   isolating and digesting bacterial (or fungal) DNA encoding 16S and
CC   23S rRNA from a sample with restriction enzymes, detecting the
CC   products, and comparing them to signature bands from a number of
CC   bacteria.  The method generates a species-conserved set of RFLP
CC   bands, unique for each species.  These species-conserved sets
CC   represent precise markers appopropriate for inter-species
CC   discriminatory purposes (i.e. to determine the species of a given,
CC   unknown isolate e.g. in a clinical specimen).  In contrast to
CC   conventional ribotyping, the present invention utilises the
CC   ribosomal operon sequences which vary less than 3% (and more
CC   preferably less than 2%) within a species and vary between species.
CC   The method is useful for medical, food, agricultural and
CC   environmental testing.  It does not require sequencing of nucleic
CC   acid from biological samples.
XX
SQ   Sequence 5519 BP; 1642 A; 1041 C; 1608 G; 1228 T; 0 other;

  Query Match             84.7%;  Score 14.4;  DB 20;  Length 5519;
  Best Local Similarity   93.8%;  Pred. No. 4.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtct 16
          ||||||||| ||||||
Db   4328 CGGGGTCTTTCCGTCT 4313


RESULT  48
AAA81533
ID   AAA81533 standard; DNA; 5669 BP.
```

```
XX
AC   AAA81533;
XX
DT   04-DEC-2000  (first entry)
XX
DE   N. meningitidis partial DNA sequence gnm_80 SEQ ID NO:80.
XX
KW   Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic;
KW   antigen; vaccine; diagnosis; infection; antibacterial; identification;
KW   Meningococcus B; MenB; ds.
XX
OS   Neisseria meningitidis.
XX
PN   WO200022430-A2.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-US23573.
XX
PR   09-OCT-1998;   98US-0103794.
PR   30-APR-1999;   99US-0132068.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Frazer CM,  Hickey E,  Peterson J,  Tettelin H,  Venter JC;
PI   Masignani V,  Galeotti C,  Mora M,  Ratti G,  Scarselli M,  Scarlato V;
PI   Rappuoli R,  Pizza M;
XX
DR   WPI; 2000-318079/27.
XX
PT   Isolated nucleotide sequences of Neisseria meningitidis which can be
PT   used in the diagnosis and treatment of N. meningitidis infection and
PT   other Neisserial infections, for example, N.gonorrhoea -
XX
PS   Claim 7; Page 1471-1473; 1760pp; English.
XX
CC   The present invention describes methods of obtaining immunogenic
CC   proteins from Neisseria genomic sequences. AAA81453 to AAA82414
CC   represent specifically claimed Neisseria meningitidis genomic DNA
CC   sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
CC   Neisseria DNA sequences and their corresponding proteins; AAA81254 to
CC   AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
CC   isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
CC   AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
CC   sequences, which are all used in the exemplification of the present
CC   invention. The nucleic acid sequences, protein sequences, and antibodies
CC   against them, can be used in the manufacture of a composition. The
CC   composition can be used as a medicament (or in the manufacture of a
CC   medicament) for treating, preventing or diagnosing infection due to
CC   Neisserial bacteria. For example, some of the identified proteins could
CC   be components of vaccines against Meningococcus B; against all serotypes;
CC   and/or against all pathogenic Neissariae. Identification of sequences
CC   from the bacterium will also facilitate production of biological probes,
CC   particularly organism-specific probes. Attempts to make efficacious
CC   Meningococcus B vaccines have failed mainly due to antigen tolerance.
CC   Multivalent vaccines have also been tried but none have successfully
CC   overcome antigenic variability. The provision of further, complete
CC   sequences may provide an opportunity to identify secreted or surface
CC   exposed proteins that may be presumed targets for the immune system and
CC   which are not antigenically variable or at least more conserved than
CC   other more variable regions.
XX
SQ   Sequence 5669 BP; 1314 A; 1627 C; 1196 G; 1532 T; 0 other;


  Query Match             84.7%;  Score 14.4;  DB 21;  Length 5669;
  Best Local Similarity   93.8%;  Pred. No. 4.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtct 16
           |||||||||| ||||||
Db    3299 cggggtctttccgtct 3314
```

```
RESULT  49
AAA60446/c
ID   AAA60446 standard; cDNA; 6585 BP.
XX
AC   AAA60446;
XX
DT   09-OCT-2000  (first entry)
XX
DE   Murine factor V encoding cDNA SEQ ID NO:4.
XX
KW   Murine; factor V; FV; activated protein C; APC; anticoagulant;
KW   activated protein C resistant factor V; thrombosis; screening;
KW   thrombophilia; ds.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             6..6557
FT                   /*tag= a
FT                   /product= "Factor V"
XX
PN   US6066778-A.
XX
PD   23-MAY-2000.
XX
PF   06-NOV-1996;   96US-0746111.
XX
PR   06-NOV-1996;   96US-0746111.
XX
PA   (UNMI ) UNIV MICHIGAN.
XX
PI   Ginsburg D,  Cui J;
XX
DR   WPI; 2000-410682/35.
DR   P-PSDB; AAB03533.
XX
PT   New transgenic mice expressing activated protein C resistant factor V
PT   and factor V null transgenic mice useful for screening anticoagulants,
PT   as models for human thrombophilia and as models for testing in utero
PT   gene therapy protocols -
XX
PS   Example 1; Fig 2; 76pp; English.
XX
CC   The present invention describes transgenic mice (I) and (II) containing
CC   modifications in the factor V gene, where (I) expresses an activated
CC   protein C (APC) resistant factor V and (II) lacks the ability to express
CC   wild-type factor V. The transgenic animals (I) and (II) are useful for
CC   screening compounds with anticoagulant activity. Methods from the present
CC   invention, and the transgenic animals, are also useful in providing
CC   models for human thrombophilia. These models are useful in providing
CC   insight into the basic regulatory mechanisms of blood coagulation and
CC   pathogenesis of human thrombosis. In addition, factor V null transgenic
CC   mice, especially pregnant females may be used as a model system to test
CC   in utero gene replacement therapy protocols. The present sequence
CC   encodes murine factor V, which is used in an example from the present
CC   invention.
XX
SQ   Sequence 6585 BP; 1946 A; 1675 C; 1432 G; 1532 T; 0 other;


  Query Match             84.7%;  Score 14.4;  DB 21;  Length 6585;
  Best Local Similarity   93.8%;  Pred. No. 4.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ggggtcttcccgtctt 17
           |||||||||| |||||
Db    2619 GGGGTCTTCCTGTCTT 2604


RESULT  50
ABL11754
ID   ABL11754 standard; cDNA; 7889 BP.
```

XX
AC ABL11754;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29744.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB67651.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 29744; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 7889 BP; 2181 A; 1606 C; 1517 G; 2585 T; 0 other;

Query Match 84.7%; Score 14.4; DB 23; Length 7889;
Best Local Similarity 93.8%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtct 16
|| ||||||||||||||
Db 6689 cgaggtcttcccgtct 6704

Search completed: September 7, 2002, 19:55:41
Job time: 4411 sec

```
RESULT 11
US-09-565-596-14/c
; Sequence 14, Application US/09565596
; Patent No. 6235484
; GENERAL INFORMATION:
;  APPLICANT:  Hogan, James J.
;  APPLICANT:  Gordon, Patricia
;  TITLE OF INVENTION:  Polynucleotide Probes for Detection and
;  TITLE OF INVENTION:  Quantitation of Actinomycetes
;  FILE REFERENCE:  GP109-02.UT
;  CURRENT APPLICATION NUMBER: US/09/565,596
;  CURRENT FILING DATE:  2000-05-03
;  PRIOR APPLICATION NUMBER:  60/132,412
;  PRIOR FILING DATE:  1999-05-03
;  NUMBER OF SEQ ID NOS:  19
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 14
;   LENGTH: 85
;   TYPE: RNA
;   ORGANISM: Frankia sp
US-09-565-596-14


  Query Match             81.2%;  Score 13.8;  DB 4;  Length 85;
  Best Local Similarity   88.2%;  Pred. No. 1e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| ||||| |
Db     85 CGGGGTCTTTCCGTCCT 69


RESULT 12
US-09-565-596-12/c
; Sequence 12, Application US/09565596
; Patent No. 6235484
; GENERAL INFORMATION:
;  APPLICANT:  Hogan, James J.
;  APPLICANT:  Gordon, Patricia
;  TITLE OF INVENTION:  Polynucleotide Probes for Detection and
;  TITLE OF INVENTION:  Quantitation of Actinomycetes
;  FILE REFERENCE:  GP109-02.UT
;  CURRENT APPLICATION NUMBER: US/09/565,596
;  CURRENT FILING DATE:  2000-05-03
;  PRIOR APPLICATION NUMBER:  60/132,412
;  PRIOR FILING DATE:  1999-05-03
;  NUMBER OF SEQ ID NOS:  19
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 12
;   LENGTH: 86
;   TYPE: RNA
;   ORGANISM: S. aureus
US-09-565-596-12


  Query Match             81.2%;  Score 13.8;  DB 4;  Length 86;
  Best Local Similarity   88.2%;  Pred. No. 1e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| ||||| |
Db     85 CGGGGTCTTTCCGTCCT 69


RESULT 13
US-09-565-596-17/c
; Sequence 17, Application US/09565596
; Patent No. 6235484
; GENERAL INFORMATION:
;  APPLICANT:  Hogan, James J.
;  APPLICANT:  Gordon, Patricia
;  TITLE OF INVENTION:  Polynucleotide Probes for Detection and
;  TITLE OF INVENTION:  Quantitation of Actinomycetes
;  FILE REFERENCE:  GP109-02.UT
;  CURRENT APPLICATION NUMBER: US/09/565,596
;  CURRENT FILING DATE:  2000-05-03
;  PRIOR APPLICATION NUMBER:  60/132,412
;  PRIOR FILING DATE:  1999-05-03
;  NUMBER OF SEQ ID NOS:  19
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 86
;   TYPE: RNA
;   ORGANISM: S. griseus
US-09-565-596-17


  Query Match             81.2%;  Score 13.8;  DB 4;  Length 86;
  Best Local Similarity   88.2%;  Pred. No. 1e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| ||||| |
Db     85 CGGGGTCTTTCCGTCCT 69


RESULT 14
US-08-371-377-21/c
; Sequence 21, Application US/08371377
; Patent No. 5851764
;  GENERAL INFORMATION:
;    APPLICANT:  Fisher, Paul B.
;    APPLICANT:  Shen, Ruoqian
;    TITLE OF INVENTION:  DEVELOPMENT OF DNA PROBES AND
;    TITLE OF INVENTION:  IMMUNOLOGICAL REAGENTS SPECIFIC FOR CELL SURFACE-EXPRESSEI
;    TITLE OF INVENTION:  MOLECULES AND TRANSFORMATION-ASSOCIATED GENES
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/371,377
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  0575/37590-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1869 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-371-377-21


  Query Match             81.2%;  Score 13.8;  DB 2;  Length 1869;
  Best Local Similarity   88.2%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy      1 cggggtcttcccgtctt 17
          ||||||||| ||||||
Db   1317 CGGGGTCTTTTCGTCTT 1301


RESULT 15
US-08-356-354-5/c
; Sequence 5, Application US/08356354
; Patent No. 5767365
;  GENERAL INFORMATION:
;    APPLICANT:  SONNEWALD, Uwe
;    TITLE OF INVENTION:  DNA SEQUENCES AND PLASMIDS FOR THE
;    TITLE OF INVENTION:  PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ostrolenk, Faber, Gerb & Soffen
;      STREET:  1180 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  US
;      ZIP:  10036-8403
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/356,354
;      FILING DATE:  20-DEC-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US PCT/EP93/01605
;      FILING DATE:  22-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P42 20 758.4
;      FILING DATE:  24-JUN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meilman, Edward A.
;      REGISTRATION NUMBER:  24,735
;      REFERENCE/DOCKET NUMBER:  P/951-105
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 382-0700
;      TELEFAX:  (212) 382-0888
;      TELEX:  236925
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2930 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Solanum tuberosum
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  118..2841
;      OTHER INFORMATION:  /note= "Sucrose-Phospahte-Synthase"
US-08-356-354-5


  Query Match             81.2%;  Score 13.8;  DB 1;  Length 2930;
  Best Local Similarity   88.2%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| || ||||
Db   1050 CGGGGTCTTTCCATCTT 1034


RESULT 16
US-08-778-656-5/c
; Sequence 5, Application US/08778656
; Patent No. 5976869
;  GENERAL INFORMATION:
;    APPLICANT:  SONNEWALD, Uwe
;    TITLE OF INVENTION:  DNA SEQUENCES AND PLASMIDS FOR THE
;    TITLE OF INVENTION:  PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ostrolenk, Faber, Gerb & Soffen
;      STREET:  1180 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  US
;      ZIP:  10036-8403
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/778,656
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/356,354
;      FILING DATE:  20-DEC-1994
;      APPLICATION NUMBER:  US PCT/EP93/01605
;      FILING DATE:  22-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P42 20 758.4
;      FILING DATE:  24-JUN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meilman, Edward A.
;      REGISTRATION NUMBER:  24,735
;      REFERENCE/DOCKET NUMBER:  P/951-105
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 382-0700
;      TELEFAX:  (212) 382-0888
;      TELEX:  236925
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2930 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Solanum tuberosum
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  118..2841
;      OTHER INFORMATION:  /note= "Sucrose-Phospahte-Synthase"
US-08-778-656-5


  Query Match             81.2%;  Score 13.8;  DB 2;  Length 2930;
  Best Local Similarity   88.2%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
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Db   1050 CGGGGTCTTTCCATCTT 1034


RESULT 17
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
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AC   AAX24985;
XX
DT   05-JUL-1999  (first entry)
XX
DE   E. coli MG1655 rrnC operon (16S-spacer-23S-spacer-5S).
XX
KW   Speciation; ribotyping; species discrimination; marker; RFLP;
KW   restriction fragment length polymorphism; bacterium; fungus;
KW   pathogen; rrnC operon; 16S RNA gene; 23S RNA gene; ds.
XX
OS   Escherichia coli.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..1541
FT                   /*tag=  a
FT                   /label= 16S
FT   misc_feature    1896..4801
FT                   /*tag=  b
FT                   /label= 23S
FT   misc_feature    4894..5013
FT                   /*tag=  c
FT                   /label= 5S
XX
PN   WO9905325-A1.
XX
PD   04-FEB-1999.
XX
PF   24-JUL-1998;   98WO-US15464.
XX
PR   25-JUL-1997;   97US-0053097.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Goldstein RN;
XX
DR   WPI; 1999-142969/12.
XX
PT   Determining species of bacteria and fungi - useful for
PT   distinguishing between bacterial/fungal species, and for determining
PT   the identity of bacterial/fungal pathogens in biological samples
XX
PS   Disclosure; Fig 7 (32/67-35/67); 133pp; English.
XX
CC   This is the DNA sequence of the Escherichia coli strain MG1655
CC   rrnC operon (16S-spacer-23S-spacer-5S).  Restriction sites for
CC   enzymes cutting the operon 5 times or less have been determined.
CC   E. coli rrnA-rrnH operon sequences are provided (see AAX24983-89).
CC   Methods and compositions are described for determining the species
CC   of an unknown bacterium or fungus in a sample.  The method involves
CC   isolating and digesting bacterial (or fungal) DNA encoding 16S and
CC   23S rRNA from a sample with restriction enzymes, detecting the
CC   products, and comparing them to signature bands from a number of
CC   bacteria.  The method generates a species-conserved set of RFLP
CC   bands, unique for each species.  These species-conserved sets
CC   represent precise markers appopropriate for inter-species
CC   discriminatory purposes (i.e. to determine the species of a given,
CC   unknown isolate e.g. in a clinical specimen).  In contrast to
CC   conventional ribotyping, the present invention utilises the
CC   ribosomal operon sequences which vary less than 3% (and more
CC   preferably less than 2%) within a species and vary between species.
CC   The method is useful for medical, food, agricultural and
CC   environmental testing.  It does not require sequencing of nucleic
CC   acid from biological samples.
XX
SQ   Sequence 5013 BP; 1310 A; 1131 C; 1533 G; 1039 T; 0 other;

  Query Match             90.6%;  Score 15.4;  DB 20;  Length 5013;
  Best Local Similarity   94.1%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtctt 17
           ||||||||| |||||||
Db    3963 CGGGGTCTTTCCGTCTT 3947


RESULT  23
AAX24987/c
ID   AAX24987 standard; DNA; 5014 BP.
XX
AC   AAX24987;
XX
DT   05-JUL-1999  (first entry)
XX
DE   E. coli MG1655 rrnE operon (16S-spacer-23S-spacer-5S).
XX
KW   Speciation; ribotyping; species discrimination; marker; RFLP;
KW   restriction fragment length polymorphism; bacterium; fungus;
KW   pathogen; rrnE operon; 16S RNA gene; 23S RNA gene; ds.
XX
OS   Escherichia coli.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..1547
FT                   /*tag=  a
FT                   /label= 16S
FT   misc_feature    1797..4819
FT                   /*tag=  b
FT                   /label= 23S
FT   misc_feature    4895..5014
FT                   /*tag=  c
FT                   /label= 5S
XX
PN   WO9905325-A1.
XX
PD   04-FEB-1999.
XX
PF   24-JUL-1998;   98WO-US15464.
XX
PR   25-JUL-1997;   97US-0053097.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Goldstein RN;
XX
DR   WPI; 1999-142969/12.
XX
PT   Determining species of bacteria and fungi - useful for
PT   distinguishing between bacterial/fungal species, and for determining
PT   the identity of bacterial/fungal pathogens in biological samples
XX
PS   Disclosure; Fig 7 (46/67-49/67); 133pp; English.
XX
CC   This is the DNA sequence of the Escherichia coli strain MG1655
CC   rrnE operon (16S-spacer-23S-spacer-5S).  Restriction sites for
CC   enzymes cutting the operon 5 times or less have been determined.
CC   E. coli rrnA-rrnH operon sequences are provided (see AAX24983-89).
CC   Methods and compositions are described for determining the species
CC   of an unknown bacterium or fungus in a sample.  The method involves
CC   isolating and digesting bacterial (or fungal) DNA encoding 16S and
CC   23S rRNA from a sample with restriction enzymes, detecting the
CC   products, and comparing them to signature bands from a number of
CC   bacteria.  The method generates a species-conserved set of RFLP
CC   bands, unique for each species.  These species-conserved sets
CC   represent precise markers appopropriate for inter-species
CC   discriminatory purposes (i.e. to determine the species of a given,
CC   unknown isolate e.g. in a clinical specimen).  In contrast to
CC   conventional ribotyping, the present invention utilises the
CC   ribosomal operon sequences which vary less than 3% (and more
CC   preferably less than 2%) within a species and vary between species.
CC   The method is useful for medical, food, agricultural and
CC   environmental testing.  It does not require sequencing of nucleic
CC   acid from biological samples.
XX
SQ   Sequence 5014 BP; 1308 A; 1129 C; 1537 G; 1040 T; 0 other;
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CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 3084 BP; 654 A; 856 C; 866 G; 707 T; 1 other;


  Query Match             90.6%;  Score 15.4;  DB 23;  Length 3084;
  Best Local Similarity   94.1%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    622 cggggtctttccgtctt 638


RESULT  20
AAH49806/c
ID   AAH49806 standard; DNA; 3118 BP.
XX
AC   AAH49806;
XX
DT   22-AUG-2001  (first entry)
XX
DE   Escherichia coli transcribed 23S rDNA-spacer-5S rDNA fragment.
XX
KW   Detection; spacer; 23S rDNA; 5S rDNA; probe; primer; phylogenetic group;
KW   enterobacterium; clinical diagnosis; food contamination; ds.
XX
OS   Escherichia coli.
XX
PN   DE19945916-A1.
XX
PD   05-APR-2001.
XX
PF   24-SEP-1999;   99DE-1045916.
XX
PR   24-SEP-1999;   99DE-1045916.
XX
PA   (BIOT-) BIOTECON DIAGNOSTICS GMBH.
XX
PI   Grabowski R,  Berghof K;
XX
DR   WPI; 2001-246133/26.
XX
PT   New nucleic acid primers and probes, useful for bacterial detection, in
PT   clinical diagnosis and detecting food contamination, comprises 23S and
PT   5S rDNA sequences -
XX
PS   Claim 1; Page 37-38; 140pp; German.
XX
CC   This invention describes a novel nucleic acid molecule (I), useful as a
CC   probe and/or primer for detecting bacteria. The invention also describes
CC   (1) a combination of at least two nucleic acids (II) for detecting
CC   bacteria or phylogenetic groups of bacteria, particularly enterobacteria;
CC   (2) a kit containing (I) or the combination of (II); (3) detecting
CC   bacteria (particularly enterobacteria) in a sample by contacting the
CC   sample with (I) or the combination of (II) and detecting hybridization;
CC   and (4) amplifying (M1) bacterial DNA from many different taxonomic
CC   groups using (I) or the combination of (II) as primers. The method is
CC   used to detect and identify bacteria, for clinical diagnosis and for
CC   detecting contamination of food. (I) can detect bacteria at various
CC   levels of selectivity (e.g.. all bacteria, particular classes, families,
CC   genera or species). The method exploits the fact that the 23S and 5S rDNA
CC   regions, and the intermediate transcribed spacer, contain some sequences
CC   that are highly conserved and others that are highly variable. This
CC   sequence represents the Escherichia coli 23S rDNA-spacer-5S rDNA region
CC   described in the method of the invention.
XX
SQ   Sequence 3118 BP; 821 A; 685 C; 976 G; 636 T; 0 other;


  Query Match             90.6%;  Score 15.4;  DB 22;  Length 3118;
  Best Local Similarity   94.1%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
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Db   2068 CGGGGTCTTTCCGTCTT 2052


RESULT  21
AAQ54682/c
ID   AAQ54682 standard; DNA; 3740 BP.
XX
AC   AAQ54682;
XX
DT   12-JUL-1994  (first entry)
XX
DE   Potato sucrose phosphate synthase.
XX
KW   Potato; Solanum tuberosum; sucrose phosphate synthase; SPS; plant;
KW   tuber; cold sweetening; ss.
XX
OS   Solanum tuberosum.
XX
FH   Key             Location/Qualifiers
FT   CDS             957..3497
FT                   /*tag=  a
FT   CDS             1203..3497
FT                   /*tag=  b
FT                   /product= SPS
XX
PN   DE4220758-A.
XX
PD   05-JAN-1994.
XX
PF   24-JUN-1992;   92DE-4220758.
XX
PR   24-JUN-1992;   92DE-4220758.
XX
PA   (GENB-) INST GENBIOLOGISCHE FORSCHUNG.
XX
PI   Sonnewald U;
XX
DR   WPI; 1994-008399/02.
DR   P-PSDB; AAR47474.
XX
PT   New DNA for potato sucrose phosphate synthase - used to generate
PT   plants having altered sucrose content, esp. those resistant to
PT   cold sweetening
XX
PS   Claim 1; Page 16-20; 23pp; German.
XX
CC   The SPS gene is used to produce plants with altered sucrose content,
CC   i.e., to increase or decrease SPS activity.  Reduction in SPS
CC   content is esp. used to reduce unwanted formation of sucrose and
CC   reducing sugars when tubers etc. are exposed to cold during storage
CC   ("cold sweetening").
XX
SQ   Sequence 3740 BP; 1062 A; 720 C; 853 G; 1105 T; 0 other;


  Query Match             90.6%;  Score 15.4;  DB 15;  Length 3740;
  Best Local Similarity   94.1%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||||| ||||
Db   1703 CGGGGTCTTCCCATCTT 1687


RESULT  22
AAX24985/c
ID   AAX24985 standard; DNA; 5013 BP.
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;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2


  Query Match            81.2%;  Score 13.8;  DB 4;  Length 4403765;
  Best Local Similarity  88.2%;  Pred. No. 54;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
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RESULT  18
US-09-626-929-7
; Sequence 7, Application US/09626929
; Patent No. 6319714
; GENERAL INFORMATION:
;  APPLICANT: CRAMERI, ANDREAS
;  APPLICANT:  STEMMER, WILLEM P.C.
;  APPLICANT:  MINSHULL, JEREMY
;  APPLICANT:  BASS, STEVEN H.
;  APPLICANT:  WELCH, MARK
;  APPLICANT:  NESS, JON E.
;  APPLICANT:  GUSTAFSSON, CLAES
;  APPLICANT:  PATTEN, PHILLIP A.
;  TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
;  FILE REFERENCE: 02-029620US
;  CURRENT APPLICATION NUMBER: US/09/626,929
;    2000-07-27
;  CURRENT FILING DATE:  2000-07-27
;  PRIOR APPLICATION NUMBER: 09/408,392
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: 60/118,813
;  PRIOR FILING DATE: 1999-02-05
;  PRIOR APPLICATION NUMBER: 60/141,049
;  PRIOR FILING DATE: 1999-06-24
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 59
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Oligonucleotide
US-09-626-929-7


  Query Match            78.8%;  Score 13.4;  DB 4;  Length 59;
  Best Local Similarity  93.3%;  Pred. No. 1.6e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db     16 gtggtcttcccgtct 30


RESULT  19
US-08-888-077A-32/c
; Sequence 32, Application US/08888077A
; Patent No. 6020143
;  GENERAL INFORMATION:
;    APPLICANT:  ST. GEORGE-HYSLOP, PETER H
;    APPLICANT:  ROMMENS, JOHANNA M
;    APPLICANT:  FRASER, PAUL E
;    TITLE OF INVENTION:  GENETIC SEQUENCES AND PROTEINS RELATED
;    TITLE OF INVENTION:  TO ALZHEIMER'S DISEASE AND USES THEREFOR.
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
;      STREET:  600 SOUTH AVENUE WEST
;      CITY:  WESTFIELD
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07090-1497
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/888,077A
;      FILING DATE:  03-JUL-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/592,541
;      FILING DATE:  26-JAN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PALISI, THOMAS M
;      REGISTRATION NUMBER:  36,629
;      REFERENCE/DOCKET NUMBER:  SCHERING 3.0-017 CIP CIP CIP IV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 654-5000
;      TELEFAX:  (908) 654-7866
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  350 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..350
;      OTHER INFORMATION:  /note= "Y2H171"
US-08-888-077A-32


  Query Match            78.8%;  Score 13.4;  DB 3;  Length 350;
  Best Local Similarity  93.3%;  Pred. No. 1.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 gggtcttcccgtctt 17
          ||||||||  ||||||
Db    292 GGGTCTTCTCGTCTT 278


RESULT  20
US-08-733-837B-1/c
; Sequence 1, Application US/08733837B
; Patent No. 6107072
;  GENERAL INFORMATION:
;    APPLICANT:  Ishida, Chika
;    TITLE OF INVENTION:  Thermostable Geranylgeranyl Diphosphate
;    TITLE OF INVENTION:  Synthase
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenyon & Kenyon
;      STREET:  One Broadway
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  US
;      ZIP:  10004
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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3+ Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS 6.2
;      SOFTWARE:  WordPerfect 6.1 Windows
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/733,837B
;      FILING DATE:  18-OCT-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-294956
;      FILING DATE:  19-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Greason, Edward W.
;      REGISTRATION NUMBER:  18,918
;      REFERENCE/DOCKET NUMBER:  77670/448
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-425-7200
;      TELEFAX:  212-425-5288
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1035 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
US-08-733-837B-1


  Query Match             78.8%;  Score 13.4;  DB 3;  Length 1035;
  Best Local Similarity   93.3%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtc 15
           ||||||||||||| |
Db     579 CGGGGTCTTCCCGAC 565


RESULT  21
US-08-224-983-1/c
; Sequence 1, Application US/08224983
; Patent No. 5646011
;  GENERAL INFORMATION:
;    APPLICANT:  Yokoyama, Shiro
;    TITLE OF INVENTION:  Cisplatin Resistance Gene and Uses Therefor
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/224,983
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Giulio A. DeConti, Jr.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  BBI-010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2564 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1599..1847
US-08-224-983-1


  Query Match             78.8%;  Score 13.4;  DB 1;  Length 2564;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 gggtcttcccgtctt 17
           ||||||||| ||||||
Db    1013 GGGTCTTCTCGTCTT 999


RESULT  22
US-08-852-933-1/c
; Sequence 1, Application US/08852933
; Patent No. 5846725
;  GENERAL INFORMATION:
;    APPLICANT:  Yokoyama, Shiro
;    TITLE OF INVENTION:  Cisplatin Resistance Gene and Uses Therefor
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/852,933
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/224,983
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Giulio A. DeConti, Jr.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  BBI-010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2564 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1599..1847
US-08-852-933-1


  Query Match             78.8%;  Score 13.4;  DB 2;  Length 2564;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 gggtcttcccgtctt 17
           ||||||||| ||||||
Db    1013 GGGTCTTCTCGTCTT 999
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;      REGISTRATION NUMBER:  29,772
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 258-5200
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12284 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Hog cholera virus
;      STRAIN:  Alfort
;      CELL LINE:  PK 15  and 38A1D
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  364..12060
;      OTHER INFORMATION:  /label= 435_kDA_protein
;    FEATURE:
;      NAME/KEY:  primer_bind
;      LOCATION:  complement (2587..2619)
;      OTHER INFORMATION:  /label= primer_1
;    FEATURE:
;      NAME/KEY:  primer_bind
;      LOCATION:  complement (2842..2880)
;      OTHER INFORMATION:  /label= primer_2
;    FEATURE:
;      NAME/KEY:  variation
;      LOCATION:  replace(127, "c")
;    FEATURE:
;      NAME/KEY:  variation
;      LOCATION:  replace(1522, "g")
;    FEATURE:
;      NAME/KEY:  variation
;      LOCATION:  replace(10989, "t")
US-09-059-853-1


  Query Match             78.8%;  Score 13.4;  DB 2;  Length 12284;
  Best Local Similarity   93.3%;  Pred. No. 2.3e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 gggtcttcccgtctt 17
          || ||||||||||||
Db   1984 GGATCTTCCCGTCTT 1970


RESULT  28
US-09-097-889-2/c
; Sequence 2, Application US/09097889
; Patent No. 6218117
;  GENERAL INFORMATION:
;    APPLICANT:  Herrnstadt, Corrina
;    APPLICANT:  Ghosh, Soumitra S.
;    APPLICANT:  Davis, Robert E.
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR IDENTIFYING
;    TITLE OF INVENTION:  AGENTS THAT QUANTATIVELY ALTER DETECTAI E
;    TITLE OF INVENTION:  EXTRAMITOCHONDRIAL DNA:  MITOCHONDRIAL DNA RATIOS
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/097,889
;      FILING DATE:  15-JUN-1998
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rosenman Ph.D., Stephen J.
;      REGISTRATION NUMBER:  43,058
;      REFERENCE/DOCKET NUMBER:  660088.417
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16569 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-097-889-2


  Query Match             78.8%;  Score 13.4;  DB 4;  Length 16569;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 gggtcttcccgtctt 17
          |||||||| ||||||
Db   2728 GGGTCTTCTCGTCTT 2714


RESULT  29
US-09-377-856-1/c
; Sequence 1, Application US/09377856
; Patent No. 6344322
; GENERAL INFORMATION:
;  APPLICANT:  Polyak, Kornelia
;  APPLICANT:  Vogelstein, Bert
;  APPLICANT:  Kinzler, Kenneth
;  TITLE OF INVENTION:  Subtle Mitochondrial Mutations as Tumor
;  TITLE OF INVENTION:  Markers
;  FILE REFERENCE:  1107.82346
;  CURRENT APPLICATION NUMBER: US/09/377,856
;  CURRENT FILING DATE:  1999-08-20
;  PRIOR APPLICATION NUMBER:  60/097,307
;  PRIOR FILING DATE:  1998-08-20
;  NUMBER OF SEQ ID NOS:  1
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 16569
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-377-856-1


  Query Match             78.8%;  Score 13.4;  DB 4;  Length 16569;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 gggtcttcccgtctt 17
          |||||||| ||||||
Db   2728 GGGTCTTCTCGTCTT 2714


RESULT  30
US-08-976-259-70/c
; Sequence 70, Application US/08976259
; Patent No. 6316609
;  GENERAL INFORMATION:
;    APPLICANT:  Dillon, Patrick J.
;    APPLICANT:  Choi, Gil H.
;    APPLICANT:  Welch, Rodney A.
;    TITLE OF INVENTION:  Nucleotide Sequence of Escherichia coli
; Patent No. 6316609
;    NUMBER OF SEQUENCES:  142
;    CORRESPONDENCE ADDRESS:
```

```
;       ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;       STREET:  1100 New York Ave, N.W., Suite 600
;       CITY:  Washington
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20005-3934
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;       COMPUTER:  HP Vectra 486/33
;       OPERATING SYSTEM:  MSDOS version 6.2
;       SOFTWARE:  ASCII Text
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/976,259
;       FILING DATE:  Herewith
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 60/031,626 AND US 60/061,953
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Steffe, Eric K.
;       REGISTRATION NUMBER:  36,688
;       REFERENCE/DOCKET NUMBER:  1488.0740002/EKS/CBM
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 371-2600
;       TELEFAX:  (202) 371-2540
;   INFORMATION FOR SEQ ID NO:  70:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  17710 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
US-08-976-259-70


  Query Match             78.8%;  Score 13.4;  DB 4;  Length 17710;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 gggtcttcccgtctt 17
          | ||||||||||||||
Db    718 GAGTCTTCCCGTCTT 704


RESULT  31
US-09-128-155-17
; Sequence 17, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
;  APPLICANT: Pan, Yang
;  TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 09404/052001
;  CURRENT APPLICATION NUMBER: US/09/128,155
;  CURRENT FILING DATE: 1998-08-03
;  EARLIER APPLICATION NUMBER: US 60/091,650
;  EARLIER FILING DATE: 1998-07-02
;  EARLIER APPLICATION NUMBER: US 60/054,646
;  EARLIER FILING DATE: 1997-08-04
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 176373
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(176373)
;   OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17


  Query Match             78.8%;  Score 13.4;  DB 3;  Length 176373;
  Best Local Similarity   93.3%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtc 15
          ||||||| ||||||||
Db  36663 cggggttttcccgtc 36677


RESULT  32
US-08-861-774E-77/c
; Sequence 77, Application US/08861774E
; Patent No. 6297007
; GENERAL INFORMATION:
;  APPLICANT: Waters, Barbara
;  APPLICANT:  Miao, Vivian
;  APPLICANT:  Ho, Yap
;  APPLICANT:  Tong, Seow
;  TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
;  TITLE OF INVENTION:  BIOACTIVE MOLECULES
;  FILE REFERENCE: 9993-006
;  CURRENT APPLICATION NUMBER: US/08/861,774E
;  CURRENT FILING DATE:  1997-05-22
;  NUMBER OF SEQ ID NOS: 94
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
;   LENGTH: 690
;   TYPE: DNA
;   ORGANISM: Usnea florida
US-08-861-774E-77


  Query Match             76.5%;  Score 13;  DB 4;  Length 690;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 gtcttcccgtctt 17
          |||||||||||||
Db    590 GTCTTCCCGTCTT 578


RESULT  33
US-08-494-714-1
; Sequence 1, Application US/08494714
; Patent No. 5587290
;  GENERAL INFORMATION:
;    APPLICANT:  Klionsky, Daniel
;    APPLICANT:  Holzer, Helmut
;    APPLICANT:  Destruelle, Monica
;    TITLE OF INVENTION:  STRESS TOLERANT YEAST MUTANTS
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
;      STREET:  4 Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/494,714
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Osman Ph.D., Richard Aron
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  A-61036/DJB/RAO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 494-8700
;      TELEFAX:  (415) 494-8771
;      TELEX:  210 277299
;  INFORMATION FOR SEQ ID NO:  1:
```

```
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/444,733
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/389,886
;      FILING DATE:  15-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/357,509
;      FILING DATE:  16-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/329,729
;      FILING DATE:  26-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/344,271
;      FILING DATE:  23-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,558
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,543
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/246,985
;      FILING DATE:  20-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0201.36/G100P11
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  92:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  195 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Clone Y5-57
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..195
US-08-444-733-92


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Qy      1 cggggtcttcccgtct 16
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Db    111 CGGGGTCTTCTCATCT 126


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; Sequence 92, Application US/08464134
; Patent No. 5849532
;  GENERAL INFORMATION:
;    APPLICANT:  Kim, Jungsuh P.
;    APPLICANT:  Wages, John
;    APPLICANT:  Young, LaVonne M.
;    APPLICANT:  Fry, Kirk E.
;    APPLICANT:  Linnen, Jeffrey M.
;    TITLE OF INVENTION:  Hepatitis G Virus and Molecular
;    TITLE OF INVENTION:  Cloning Thereof
;    NUMBER OF SEQUENCES:  277
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,134
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/389,886
;      FILING DATE:  15-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/357,509
;      FILING DATE:  16-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/329,729
;      FILING DATE:  26-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/344,271
;      FILING DATE:  23-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,558
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,543
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/246,985
;      FILING DATE:  20-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0201.36/G100P11
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  92:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  195 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Clone Y5-57
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..195
US-08-464-134-92


  Query Match           75.3%;  Score 12.8;  DB 2;  Length 195;
  Best Local Similarity  87.5%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy      1 cggggtcttcccgtct 16
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Db    111 CGGGGTCTTCTCATCT 126


RESULT  41
US-08-461-361-92
; Sequence 92, Application US/08461361
; Patent No. 5856134
;  GENERAL INFORMATION:
;    APPLICANT:  Kim, Jungsuh P.
;    APPLICANT:  Wages, John
;    APPLICANT:  Young, LaVonne M.
;    APPLICANT:  Fry, Kirk E.
;    APPLICANT:  Linnen, Jeffrey M.
;    TITLE OF INVENTION:  Hepatitis G Virus and Molecular
;    TITLE OF INVENTION:  Cloning Thereof
;    NUMBER OF SEQUENCES:  277
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,361
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/389,886
;      FILING DATE:  15-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/357,509
;      FILING DATE:  16-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/329,729
;      FILING DATE:  26-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/344,271
;      FILING DATE:  23-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,558
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,543
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/246,985
;      FILING DATE:  20-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0201.36/G100P11
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  92:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  195 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Clone Y5-57
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..195
US-08-461-361-92


  Query Match             75.3%;  Score 12.8;  DB 2;  Length 195;
  Best Local Similarity   87.5%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtct 16
          ||||||||||  | |||
Db    111 CGGGGTCTTCTCATCT 126


RESULT  42
US-08-485-910-92
; Sequence 92, Application US/08485910
; Patent No. 5874563
;  GENERAL INFORMATION:
;    APPLICANT:  Kim, Jungsuh P.
;    APPLICANT:  Wages, John
;    APPLICANT:  Young, LaVonne M.
;    APPLICANT:  Fry, Kirk E.
;    APPLICANT:  Linnen, Jeffrey M.
;    TITLE OF INVENTION:  Hepatitis G Virus and Molecular
;    TITLE OF INVENTION:  Cloning Thereof
;    NUMBER OF SEQUENCES:  277
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,910
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/389,886
;      FILING DATE:  15-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/357,509
;      FILING DATE:  16-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/329,729
;      FILING DATE:  26-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/344,271
;      FILING DATE:  23-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,558
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,543
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/246,985
;      FILING DATE:  20-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0201.36/G100P11
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
```

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;  INFORMATION FOR SEQ ID NO:  92:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  195 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Clone Y5-57
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..195
US-08-485-910-92


  Query Match             75.3%;  Score 12.8;  DB 2;  Length 195;
  Best Local Similarity   87.5%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtct 16
          |||||||||| | |||
Db    111 CGGGGTCTTCTCATCT 126


RESULT  43
PCT-US95-06266-76
; Sequence 76, Application PC/TUS9506266
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Detection of Viral Antigens Coded
;    TITLE OF INVENTION:  by Reverse Reading Frames
;    NUMBER OF SEQUENCES:  157
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Avenue, Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06266
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/246,985
;      FILING DATE:  20-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,561
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/329,729
;      FILING DATE:  26-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/344,271
;      FILING DATE:  23-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/357,509
;      FILING DATE:  16-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/389,886
;      FILING DATE:  15-FEB-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0202.41
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  76:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  195 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Clone Y5-57
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..195
PCT-US95-06266-76


  Query Match             75.3%;  Score 12.8;  DB 5;  Length 195;
  Best Local Similarity   87.5%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtct 16
          |||||||||| | |||
Db    111 CGGGGTCTTCTCATCT 126


RESULT  44
US-08-466-033-19
; Sequence 19, Application US/08466033
; Patent No. 5766840
;  GENERAL INFORMATION:
;    APPLICANT:  Kim, Jungsuh P.
;    APPLICANT:  Wages, John
;    APPLICANT:  Young, LaVonne M.
;    APPLICANT:  Fry, Kirk E.
;    APPLICANT:  Linnen, Jeffrey M.
;    TITLE OF INVENTION:  Hepatitis G Virus and Molecular
;    TITLE OF INVENTION:  Cloning Thereof
;    NUMBER OF SEQUENCES:  277
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/466,033
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/389,886
;      FILING DATE:  15-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/357,509
;      FILING DATE:  16-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/329,729
;      FILING DATE:  26-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/344,271
;      FILING DATE:  23-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,558
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  US 08/285,543
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/246,985
;      FILING DATE:  20-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0201.36/G100P11
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  203 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  470-20-1 CLONE, WITHOUT SISPA
;      INDIVIDUAL ISOLATE:  LINKERS
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2..203
US-08-466-033-19


  Query Match             75.3%;  Score 12.8;  DB 1;  Length 203;
  Best Local Similarity   87.5%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtct 16
           |||||||||| | |||
Db      73 CGGGGTCTTCTCATCT 88


RESULT  45
US-08-444-733-19
; Sequence 19, Application US/08444733
; Patent No. 5824507
;  GENERAL INFORMATION:
;    APPLICANT:  Kim, Jungsuh P.
;    APPLICANT:  Wages, John
;    APPLICANT:  Young, LaVonne M.
;    APPLICANT:  Fry, Kirk E.
;    APPLICANT:  Linnen, Jeffrey M.
;    TITLE OF INVENTION:  Hepatitis G Virus and Molecular
;    TITLE OF INVENTION:  Cloning Thereof
;    NUMBER OF SEQUENCES:  277
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/444,733
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/389,886
;      FILING DATE:  15-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/357,509
;      FILING DATE:  16-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/329,729
;      FILING DATE:  26-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/344,271
;      FILING DATE:  23-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,558
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,543
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/246,985
;      FILING DATE:  20-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0201.36/G100P11
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  203 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  470-20-1 CLONE, WITHOUT SISPA
;      INDIVIDUAL ISOLATE:  LINKERS
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2..203
US-08-444-733-19


  Query Match             75.3%;  Score 12.8;  DB 1;  Length 203;
  Best Local Similarity   87.5%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtct 16
           |||||||||| | |||
Db      73 CGGGGTCTTCTCATCT 88


RESULT  46
US-08-464-134-19
; Sequence 19, Application US/08464134
; Patent No. 5849532
;  GENERAL INFORMATION:
;    APPLICANT:  Kim, Jungsuh P.
;    APPLICANT:  Wages, John
;    APPLICANT:  Young, LaVonne M.
;    APPLICANT:  Fry, Kirk E.
;    APPLICANT:  Linnen, Jeffrey M.
;    TITLE OF INVENTION:  Hepatitis G Virus and Molecular
;    TITLE OF INVENTION:  Cloning Thereof
;    NUMBER OF SEQUENCES:  277
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,134
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/389,886
;      FILING DATE:  15-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/357,509
;      FILING DATE:  16-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/329,729
;      FILING DATE:  26-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/344,271
;      FILING DATE:  23-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,558
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,543
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/246,985
;      FILING DATE:  20-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0201.36/G100P11
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  203 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  470-20-1 CLONE, WITHOUT SISPA
;      INDIVIDUAL ISOLATE:  LINKERS
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2..203
US-08-464-134-19


  Query Match             75.3%;  Score 12.8;  DB 2;  Length 203;
  Best Local Similarity   87.5%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtct 16
          |||||||||| | |||
Db     73 CGGGGTCTTCTCATCT 88


RESULT  47
US-08-461-361-19
; Sequence 19, Application US/08461361
; Patent No. 5856134
;  GENERAL INFORMATION:
;    APPLICANT:  Kim, Jungsuh P.
;    APPLICANT:  Wages, John
;    APPLICANT:  Young, LaVonne M.
;    APPLICANT:  Fry, Kirk E.
;    APPLICANT:  Linnen, Jeffrey M.
;    TITLE OF INVENTION:  Hepatitis G Virus and Molecular
;    TITLE OF INVENTION:  Cloning Thereof
;    NUMBER OF SEQUENCES:  277
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,361
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/389,886
;      FILING DATE:  15-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/357,509
;      FILING DATE:  16-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/329,729
;      FILING DATE:  26-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/344,271
;      FILING DATE:  23-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,558
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,543
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/246,985
;      FILING DATE:  20-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0201.36/G100P11
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  203 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  470-20-1 CLONE, WITHOUT SISPA
;      INDIVIDUAL ISOLATE:  LINKERS
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2..203
US-08-461-361-19


  Query Match             75.3%;  Score 12.8;  DB 2;  Length 203;
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  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtct 16
          |||||||||| | |||
Db     73 CGGGGTCTTCTCATCT 88


RESULT  48
US-08-485-910-19
; Sequence 19, Application US/08485910
; Patent No. 5874563
;  GENERAL INFORMATION:
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;    APPLICANT:  Kim, Jungsuh P.
;    APPLICANT:  Wages, John
;    APPLICANT:  Young, LaVonne M.
;    APPLICANT:  Fry, Kirk E.
;    APPLICANT:  Linnen, Jeffrey M.
;    TITLE OF INVENTION:  Hepatitis G Virus and Molecular
;    TITLE OF INVENTION:  Cloning Thereof
;    NUMBER OF SEQUENCES:  277
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,910
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/389,886
;      FILING DATE:  15-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/357,509
;      FILING DATE:  16-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/329,729
;      FILING DATE:  26-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/344,271
;      FILING DATE:  23-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,558
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,543
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/246,985
;      FILING DATE:  20-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0201.36/G100P11
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  203 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  470-20-1 CLONE, WITHOUT SISPA
;      INDIVIDUAL ISOLATE:  LINKERS
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2..203
US-08-485-910-19


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  Best Local Similarity  87.5%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtct 16
           |||||||||| | |||
Db      73 CGGGGTCTTCTCATCT 88


RESULT  49
PCT-US95-06266-19
; Sequence 19, Application PC/TUS9506266
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Detection of Viral Antigens Coded
;    TITLE OF INVENTION:  by Reverse Reading Frames
;    NUMBER OF SEQUENCES:  157
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Avenue, Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06266
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/246,985
;      FILING DATE:  20-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,561
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/329,729
;      FILING DATE:  26-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/344,271
;      FILING DATE:  23-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/357,509
;      FILING DATE:  16-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/389,886
;      FILING DATE:  15-FEB-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0202.41
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  203 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  470-20-1 CLONE, WITHOUT SISPA
;      INDIVIDUAL ISOLATE:  LINKERS
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2..203
PCT-US95-06266-19


  Query Match           75.3%;  Score 12.8;  DB 5;  Length 203;
  Best Local Similarity  87.5%;  Pred. No. 3.5e+02;
```

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  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtct 16
           |||||||||| | |||
Db      73 CGGGGTCTTCTCATCT 88


RESULT  50
US-08-466-033-3
; Sequence 3, Application US/08466033
; Patent No. 5766840
;  GENERAL INFORMATION:
;    APPLICANT:  Kim, Jungsuh P.
;    APPLICANT:  Wages, John
;    APPLICANT:  Young, LaVonne M.
;    APPLICANT:  Fry, Kirk E.
;    APPLICANT:  Linnen, Jeffrey M.
;    TITLE OF INVENTION:  Hepatitis G Virus and Molecular
;    TITLE OF INVENTION:  Cloning Thereof
;    NUMBER OF SEQUENCES:  277
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/466,033
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/389,886
;      FILING DATE:  15-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/357,509
;      FILING DATE:  16-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/329,729
;      FILING DATE:  26-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/344,271
;      FILING DATE:  23-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,558
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/285,543
;      FILING DATE:  03-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/246,985
;      FILING DATE:  20-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0201.36/G100P11
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  237 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  PNF 2161 CLONE 470-20-1
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..237
US-08-466-033-3


  Query Match             75.3%;  Score 12.8;  DB 1;  Length 237;
  Best Local Similarity   87.5%;  Pred. No. 3.6e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtct 16
           |||||||||| | |||
Db      90 CGGGGTCTTCTCATCT 105


Search completed: September  7, 2002, 19:53:00
Job time: 7600 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 17:40:55 ; Search time 1771.06 Seconds
(without alignments)
129.554 Million cell updates/sec

Title: US-09-673-645A-1
Perfect score: 17
Sequence: 1 cggggtcttcccgtctt 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	15.4	90.6	158	9	AV428414	AV428414 AV428414
c	2	15.4	90.6	201	9	AV406641	AV406641 AV406641
c	3	15.4	90.6	217	9	AV413069	AV413069 AV413069
c	4	15.4	90.6	220	9	AW165921	AW165921 JAA000397
c	5	15.4	90.6	248	9	AT000506	AT000506 AT000506
c	6	15.4	90.6	263	9	AV417186	AV417186 AV417186
c	7	15.4	90.6	271	9	BB158339	BB158339 BB158339
c	8	15.4	90.6	284	9	AV425293	AV425293 AV425293
c	9	15.4	90.6	307	9	AI168885	AI168885 JA00A025.
c	10	15.4	90.6	362	9	AI941851	AI941851 JAA000262
c	11	15.4	90.6	379	9	AV414457	AV414457 AV414457
c	12	15.4	90.6	385	9	AI932079	AI932079 JAA000221
	13	15.4	90.6	386	10	BI119300	BI119300 AR026H02P
c	14	15.4	90.6	398	9	AV412952	AV412952 AV412952
c	15	15.4	90.6	399	9	AI168886	AI168886 JA00A031.
c	16	15.4	90.6	401	9	AV416711	AV416711 AV416711
c	17	15.4	90.6	413	9	AI168905	AI168905 JA00A150.
c	18	15.4	90.6	414	9	AV414502	AV414502 AV414502
c	19	15.4	90.6	418	9	AI168891	AI168891 JA00A137.
c	20	15.4	90.6	419	9	AI168893	AI168893 JA00A154.
c	21	15.4	90.6	421	9	AV428402	AV428402 AV428402
c	22	15.4	90.6	425	9	AV426304	AV426304 AV426304
c	23	15.4	90.6	427	9	AW707310	AW707310 JAA000647
c	24	15.4	90.6	433	9	AW736775	AW736775 JAYL0254.
c	25	15.4	90.6	437	10	BF327832	BF327832 PM0-BN014
	26	15.4	90.6	439	10	BG810759	BG810759 daf30h02.
c	27	15.4	90.6	442	9	AV423171	AV423171 AV423171
	28	15.4	90.6	451	10	BE345961	BE345961 JAA000767
c	29	15.4	90.6	475	9	AW736765	AW736765 JAYG00039
c	30	15.4	90.6	483	10	BE819808	BE819808 JAYB0164.
c	31	15.4	90.6	484	9	AW707291	AW707291 JAA000628
c	32	15.4	90.6	500	9	AV428939	AV428939 AV428939
c	33	15.4	90.6	505	9	BE123840	BE123840 JAYB0147.
	34	15.4	90.6	506	10	BI403676	BI403676 MI-P-CP1-
	35	15.4	90.6	512	9	AW786990	AW786990 120660 MA
	36	15.4	90.6	517	9	AU216075	AU216075 AU216075
c	37	15.4	90.6	523	9	AI932095	AI932095 JAA000237
c	38	15.4	90.6	554	9	AW329878	AW329878 JAYL0232.
c	39	15.4	90.6	555	9	AW231233	AW231233 JAYH0020.
c	40	15.4	90.6	555	9	BE187680	BE187680 JAYG0068.
c	41	15.4	90.6	558	10	BE819807	BE819807 JAYB0176.
c	42	15.4	90.6	563	9	AW191455	AW191455 JAA000486
c	43	15.4	90.6	585	9	AW225509	AW225509 JAA000526
c	44	15.4	90.6	592	10	BF713615	BF713615 JAYS0031.
c	45	15.4	90.6	606	9	AT006807	AT006807 AT006807
c	46	15.4	90.6	625	9	AW186560	AW186560 JAA000460
	47	15.4	90.6	628	10	BI183250	BI183250 UNL-P-FN-
	48	15.4	90.6	642	12	AQ989715	AQ989715 Rfc00343
c	49	15.4	90.6	654	9	AW225508	AW225508 JAA000525
c	50	15.4	90.6	658	9	AI942193	AI942193 JAA000355

ALIGNMENTS

RESULT 1
AV428414/c
LOCUS AV428414 158 bp mRNA linear EST 23-MAY-2000
DEFINITION AV428414 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWM096h03_r 5', mRNA sequence.
ACCESSION AV428414
VERSION AV428414.1 GI:7789345
KEYWORDS EST.
SOURCE Lotus japonicus.
ORGANISM Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
REFERENCE 1 (bases 1 to 158)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
JOURNAL DNA Res. 7 (2), 127-130 (2000)
MEDLINE 20277479
COMMENT Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES Location/Qualifiers
source 1. .158
/organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone="MWM096h03_r"
/clone_lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI; isolate=Miyakojima MG-20"
BASE COUNT 42 a 43 c 40 g 33 t

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ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 9;  Length 158;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    120 CGGGGTCTTACCGTCTT 104


RESULT   2
AV406641/c
LOCUS       AV406641                201 bp    mRNA    linear   EST 23-MAY-2000
DEFINITION  AV406641 Lotus japonicus young plants (two-week old) Lotus
            japonicus cDNA clone MWL007e03_r 5', mRNA sequence.
ACCESSION   AV406641
VERSION     AV406641.1  GI:7719495
KEYWORDS    EST.
SOURCE      Lotus japonicus.
  ORGANISM  Lotus japonicus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
            Lotus.
REFERENCE   1  (bases 1 to 201)
  AUTHORS   Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  TITLE     Generation of 7137 non-redundant expressed sequence tags from a
            legume, Lotus japonicus
  JOURNAL   DNA Res. 7 (2), 127-130 (2000)
  MEDLINE   20277479
COMMENT     Contact: Yasukazu Nakamura
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .201
                     /organism="Lotus japonicus"
                     /db_xref="taxon:34305"
                     /clone="MWL007e03_r"
                     /clone_lib="Lotus japonicus young plants (two-week old)"
                     /dev_stage="young plants (two-week old)"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI; isolate=Miyakojima MG-20"
BASE COUNT       53 a     54 c     51 g     43 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 9;  Length 201;
  Best Local Similarity   94.1%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    167 CGGGGTCTTACCGTCTT 151


RESULT   3
AV413069/c
LOCUS       AV413069                217 bp    mRNA    linear   EST 23-MAY-2000
DEFINITION  AV413069 Lotus japonicus young plants (two-week old) Lotus
            japonicus cDNA clone MWM227h10_r 5', mRNA sequence.
ACCESSION   AV413069
VERSION     AV413069.1  GI:7742245
KEYWORDS    EST.
SOURCE      Lotus japonicus.
  ORGANISM  Lotus japonicus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
            Lotus.
REFERENCE   1  (bases 1 to 217)
  AUTHORS   Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  TITLE     Generation of 7137 non-redundant expressed sequence tags from a
            legume, Lotus japonicus
  JOURNAL   DNA Res. 7 (2), 127-130 (2000)
  MEDLINE   20277479
COMMENT     Contact: Yasukazu Nakamura
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .217
                     /organism="Lotus japonicus"
                     /db_xref="taxon:34305"
                     /clone="MWM227h10_r"
                     /clone_lib="Lotus japonicus young plants (two-week old)"
                     /dev_stage="young plants (two-week old)"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI; isolate=Miyakojima MG-20"
BASE COUNT       61 a     53 c     59 g     44 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 9;  Length 217;
  Best Local Similarity   94.1%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db     75 CGGGGTCTTACCGTCTT 59


RESULT   4
AW165921/c
LOCUS       AW165921                220 bp    mRNA    linear   EST 20-MAR-2000
DEFINITION  JAA000397.SH3 Adult SjC 7/94 Schistosoma japonicum cDNA 5', mRNA
            sequence.
ACCESSION   AW165921
VERSION     AW165921.1  GI:6382852
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 220)
  AUTHORS   Hu,W., Brindley,P.J. and Feng,Z.
  TITLE     Expressed sequence tags from adults of Schistosoma japonicum (Anhui
            strain) (Hu, Brindley, Feng)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Brindley, P.J.
            Molecular Parasitology Unit
            Queensland Institute of Medical Research
            300 Herston Road, Qeensland 4029, Australia
            Tel: 61 7 3362 0413
            Fax: 61 7 3362 0104
            Email: paulB@qimr.edu.au
            PCR PRimers
            FORWARD: M13 Forward
            BACKWARD: M13 Reverse
            Insert Length: 1   Std Error: 0.00
            Seq primer: T3 Reverse
            High quality sequence stop: 156.
FEATURES             Location/Qualifiers
     source          1. .220
                     /organism="Schistosoma japonicum"
                     /strain="Chinese (Anhui) strain"
                     /db_xref="taxon:6182"
                     /clone_lib="Adult SjC 7/94"
                     /sex="Male and female"
                     /tissue_type="Whole body"
                     /dev_stage="Adult worms"
                     /lab_host="Mouse and rabbit"
```

/note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2: Xhol I; Several hundred adult Schistosoma japonicum (Anhui , P.R. China, strain), of mixed sex, were perfused from the mesenteries of experimentally infected mice and rabbits at the Queensland Institute of Medical Research, Brisbane, Australia (QIMR), and stored for several months in liquid nitrogen. Subsequently, mRNA was isolated at the QIMR from lysates of these worms by oligo dT chromatography, using a kit from Pharmacia. The mRNA was then shipped to Clontech, Palo Alto, CA, USA, who constructed a cDNA library. First strand synthesis was primed with an oligo-dT-XhoI-primer and synthesized using M-MLV reverse transcriptase. Second strand synthesis was accomplished with RNAse H and T4 DNA polymerase. The double stranded cDNA was ligated to EcoRI linkers, digested with EcoRI and XhoI, and ligated into the phagemid vector lambda ZAP II XR. After construction of this directional library by Clontech, it was returned to the QIMR. During analysis of the library at the QIMR, we have found that a small percentage, 2% to 3%, of the clones contain inserts that appear to be highly homologous to sequences from salmonoid fishes, as determined by homology comparisons using BLAST and by Southern hybridization analysis to genomic DNA from salmon (Sigma Chemical Co., St. Louis, MO) under stringent washing conditions. The remainder of the clones appear to contain S. japonicum sequences."

```
BASE COUNT       67 a     26 c     48 g     79 t
ORIGIN
```

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  Query Match             90.6%;  Score 15.4;  DB 9;  Length 220;
  Best Local Similarity   94.1%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    182 CGGGGTCTTTCCGTCTT 166
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```
RESULT   5
AT000506/c
LOCUS       AT000506                248 bp    mRNA    linear   EST 13-AUG-1998
DEFINITION  AT000506 Brassica rapa guard cell Brassica rapa subsp. pekinensis
            cDNA clone DGT252, mRNA sequence.
ACCESSION   AT000506
VERSION     AT000506.1  GI:3414040
KEYWORDS    EST.
SOURCE      Brassica rapa subsp. pekinensis.
  ORGANISM  Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 248)
  AUTHORS   Kwak,J.M., Kim,S.A., Hong,S.W. and Nam,H.G.
  TITLE     Evaluation of 515 expressed sequence tags obtained from guard cells
            of Brassica campestris
  JOURNAL   Planta 202 (1), 9-17 (1997)
  MEDLINE   97320163
COMMENT     Contact: Hong-Gil Nam
            Department of Life Science, Plant Molecular Genetics Laboratory
            Pohang University of Science and Technology
            San 31 Hyojadong, Pohang Kyungbuk 790-784, Korea
            Email: hgn@bric.postech.ac.kr
            Submitted through BRIC(Biological Research Information Center) of
            Korea URL: http://bric.postech.ac.kr/.
FEATURES             Location/Qualifiers
     source          1. .248
                     /organism="Brassica rapa subsp. pekinensis"
                     /db_xref="taxon:51351"
                     /clone="DGT252"
                     /clone_lib="Brassica rapa guard cell"
                     /cell_type="guard cell protoplast"
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BASE COUNT       61 a     59 c     67 g     57 t      4 others
ORIGIN
```

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  Query Match             90.6%;  Score 15.4;  DB 9;  Length 248;
  Best Local Similarity   94.1%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db     98 CGGGGTCTTTCCGTCTT 82
```

```
RESULT   6
AV417186/c
LOCUS       AV417186                263 bp    mRNA    linear   EST 23-MAY-2000
DEFINITION  AV417186 Lotus japonicus young plants (two-week old) Lotus
            japonicus cDNA clone MWM140e05_r 5', mRNA sequence.
ACCESSION   AV417186
VERSION     AV417186.1  GI:7746364
KEYWORDS    EST.
SOURCE      Lotus japonicus.
  ORGANISM  Lotus japonicus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
            Lotus.
REFERENCE   1  (bases 1 to 263)
  AUTHORS   Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  TITLE     Generation of 7137 non-redundant expressed sequence tags from a
            legume, Lotus japonicus
  JOURNAL   DNA Res. 7 (2), 127-130 (2000)
  MEDLINE   20277479
COMMENT     Contact: Yasukazu Nakamura
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .263
                     /organism="Lotus japonicus"
                     /db_xref="taxon:34305"
                     /clone="MWM140e05_r"
                     /clone_lib="Lotus japonicus young plants (two-week old)"
                     /dev_stage="young plants (two-week old)"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI; isolate=Miyakojima MG-20"
BASE COUNT       71 a     64 c     73 g     55 t
ORIGIN
```

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  Query Match             90.6%;  Score 15.4;  DB 9;  Length 263;
  Best Local Similarity   94.1%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    248 CGGGGTCTTACCGTCTT 232
```

```
RESULT   7
BB158339/c
LOCUS       BB158339                271 bp    mRNA    linear   EST 29-JUN-2000
DEFINITION  BB158339 RIKEN full-length enriched, 16 days neonate thymus Mus
            musculus cDNA clone A130040C01 3' similar to U15635 Mus musculus
            IFN-gamma induced (Mg11) mRNA, mRNA sequence.
ACCESSION   BB158339
VERSION     BB158339.1  GI:8814269
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
REFERENCE   1  (bases 1 to 271)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
            , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
            , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.
            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
            ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
            , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
            ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .271
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="A130040C01"
                     /clone_lib="RIKEN full-length enriched, 16 days neonate
                     thymus"
                     /tissue_type="thymus"
                     /dev_stage="16 days neonate"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 185.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cleaved with XhoI and BamHI. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I."
BASE COUNT       84 a     70 c     50 g     67 t
ORIGIN

  Query Match             90.6%;  Score 15.4;  DB 9;  Length 271;
  Best Local Similarity   94.1%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          | ||||||||||||||||
Db    103 CAGGGTCTTCCCGTCTT 87


RESULT   8
AV425293/c
LOCUS       AV425293                 284 bp    mRNA    linear   EST 23-MAY-2000
DEFINITION  AV425293 Lotus japonicus young plants (two-week old) Lotus
            japonicus cDNA clone MWM051h09_r 5', mRNA sequence.
ACCESSION   AV425293
VERSION     AV425293.1  GI:7783087
KEYWORDS    EST.
SOURCE      Lotus japonicus.
  ORGANISM  Lotus japonicus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
            Lotus.
REFERENCE   1  (bases 1 to 284)
  AUTHORS   Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  TITLE     Generation of 7137 non-redundant expressed sequence tags from a
            legume, Lotus japonicus
  JOURNAL   DNA Res. 7 (2), 127-130 (2000)
  MEDLINE   20277479
COMMENT     Contact: Yasukazu Nakamura
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .284
                     /organism="Lotus japonicus"
                     /db_xref="taxon:34305"
                     /clone="MWM051h09_r"
                     /clone_lib="Lotus japonicus young plants (two-week old)"
                     /dev_stage="young plants (two-week old)"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI; isolate=Miyakojima MG-20"
BASE COUNT       77 a     68 c     80 g     59 t
ORIGIN

  Query Match             90.6%;  Score 15.4;  DB 9;  Length 284;
  Best Local Similarity   94.1%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    275 CGGGGTCTTACCGTCTT 259


RESULT   9
AI168885/c
LOCUS       AI168885                 307 bp    mRNA    linear   EST 05-OCT-1998
DEFINITION  JA00A025.QA3 Adult SjC 7/94 Schistosoma japonicum cDNA clone
            SJADA25 5' similar to Ribosomal RNA (mt), mRNA sequence.
ACCESSION   AI168885
VERSION     AI168885.1  GI:3702055
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 307)
  AUTHORS   Brindley,P.J. and Fan,J.
  TITLE     ESTs from Adults of Schistosoma japonicum (Anhui strain)
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Brindley, P.J.
            Molecular Parasitology Unit
            Queensland Institute of Medical Research
            300 Herston Road, Qeensland 4029, Australia
```

```
            Tel: 61 7 3362 0413
            Fax: 61 7 3362 0104
            Email: paulB@qimr.edu.au
            PCR PRimers
            FORWARD: M13 Forward
            BACKWARD: M13 Reverse
            Insert Length: 900   Std Error: 0.00
            Seq primer: T3 Reverse
            High quality sequence stop: 307.
FEATURES             Location/Qualifiers
     source          1. .307
                     /organism="Schistosoma japonicum"
                     /strain="Chinese (Anhui) strain"
                     /db_xref="taxon:6182"
                     /clone="SJADA25"
                     /clone_lib="Adult SjC 7/94"
                     /sex="Male and female"
                     /tissue_type="Whole body"
                     /dev_stage="Adult worms"
                     /lab_host="Mouse and rabbit"
                     /note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
                     Xhol I; Several hundred adult Schistosoma japonicum (Anhui
                     , P.R. China, strain), of mixed sex, were perfused from
                     the mesenteries of experimentally infected mice and
                     rabbits at the Queensland Institute of Medical Research,
                     Brisbane, Australia (QIMR), and stored for several months
                     in liquid nitrogen. Subsequently, mRNA was isolated at the
                     QIMR from lysates of these worms by oligo dT
                     chromatography, using a kit from Pharmacia. The mRNA was
                     then shipped to Clontech, Palo Alto, CA, USA, who
                     constructed a cDNA library. First strand synthesis was
                     primed with an oligo-dT-XhoI-primer and synthesized using
                     M-MLV reverse transcriptase. Second strand synthesis was
                     accomplished with RNAse H and T4 DNA polymerase. The
                     double stranded cDNA was ligated to EcoRI linkers,
                     digested with EcoRI and XhoI, and ligated into the
                     phagemid vector lambda ZAP II XR. After construction of
                     this directional library by Clontech, it was returned to
                     the QIMR. During analysis of the library at the QIMR, we
                     have found that a small percentage, 2% to 3%, of the
                     clones contain inserts that appear to be highly homologous
                     to sequences from salmonoid fishes, as determined by
                     homology comparisons using BLAST and by Southern
                     hybridization analysis to genomic DNA from salmon (Sigma
                     Chemical Co., St. Louis, MO) under stringent washing
                     conditions. The remainder of the clones appear to contain
                     S. japonicum sequences."
BASE COUNT       95 a     35 c     60 g    117 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 9;  Length 307;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    306 CGGGGTCTTTCCGTCTT 290


RESULT  10
AI941851/c
LOCUS       AI941851                 362 bp    mRNA    linear   EST 20-MAR-2000
DEFINITION  JAA000262.SH3 Adult SjC 7/94 Schistosoma japonicum cDNA 5', mRNA
            sequence.
ACCESSION   AI941851
VERSION     AI941851.1  GI:5701631
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 362)
  AUTHORS   Hu,W., Brindley,P.J. and Feng,Z.
  TITLE     Expressed sequence tags from adults of Schistosoma japonicum (Anhui
            strain) (Hu, Brindley, Feng)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Brindley, P.J.
            Molecular Parasitology Unit
            Queensland Institute of Medical Research
            300 Herston Road, Qeensland 4029, Australia
            Tel: 61 7 3362 0413
            Fax: 61 7 3362 0104
            Email: paulB@qimr.edu.au
            PCR PRimers
            FORWARD: M13 Forward
            BACKWARD: M13 Reverse
            Insert Length: 600   Std Error: 0.00
            Seq primer: T3 Reverse
            High quality sequence stop: 362.
FEATURES             Location/Qualifiers
     source          1. .362
                     /organism="Schistosoma japonicum"
                     /strain="Chinese (Anhui) strain"
                     /db_xref="taxon:6182"
                     /clone_lib="Adult SjC 7/94"
                     /sex="Male and female"
                     /tissue_type="Whole body"
                     /dev_stage="Adult worms"
                     /lab_host="Mouse and rabbit"
                     /note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
                     Xhol I; Several hundred adult Schistosoma japonicum (Anhui
                     , P.R. China, strain), of mixed sex, were perfused from
                     the mesenteries of experimentally infected mice and
                     rabbits at the Queensland Institute of Medical Research,
                     Brisbane, Australia (QIMR), and stored for several months
                     in liquid nitrogen. Subsequently, mRNA was isolated at the
                     QIMR from lysates of these worms by oligo dT
                     chromatography, using a kit from Pharmacia. The mRNA was
                     then shipped to Clontech, Palo Alto, CA, USA, who
                     constructed a cDNA library. First strand synthesis was
                     primed with an oligo-dT-XhoI-primer and synthesized using
                     M-MLV reverse transcriptase. Second strand synthesis was
                     accomplished with RNAse H and T4 DNA polymerase. The
                     double stranded cDNA was ligated to EcoRI linkers,
                     digested with EcoRI and XhoI, and ligated into the
                     phagemid vector lambda ZAP II XR. After construction of
                     this directional library by Clontech, it was returned to
                     the QIMR. During analysis of the library at the QIMR, we
                     have found that a small percentage, 2% to 3%, of the
                     clones contain inserts that appear to be highly homologous
                     to sequences from salmonoid fishes, as determined by
                     homology comparisons using BLAST and by Southern
                     hybridization analysis to genomic DNA from salmon (Sigma
                     Chemical Co., St. Louis, MO) under stringent washing
                     conditions. The remainder of the clones appear to contain
                     S. japonicum sequences."
BASE COUNT      107 a     43 c     80 g    132 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 9;  Length 362;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db     31 CGGGGTCTTTCCGTCTT 15


RESULT  11
AV414457/c
LOCUS       AV414457                 379 bp    mRNA    linear   EST 23-MAY-2000
DEFINITION  AV414457 Lotus japonicus young plants (two-week old) Lotus
            japonicus cDNA clone MWM244h04_r 5', mRNA sequence.
ACCESSION   AV414457
```

```
VERSION     AV414457.1  GI:7743633
KEYWORDS    EST.
SOURCE      Lotus japonicus.
  ORGANISM  Lotus japonicus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
            Lotus.
REFERENCE   1  (bases 1 to 379)
  AUTHORS   Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  TITLE     Generation of 7137 non-redundant expressed sequence tags from a
            legume, Lotus japonicus
  JOURNAL   DNA Res. 7 (2), 127-130 (2000)
  MEDLINE   20277479
COMMENT     Contact: Yasukazu Nakamura
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .379
                     /organism="Lotus japonicus"
                     /db_xref="taxon:34305"
                     /clone="MWM244h04_r"
                     /clone_lib="Lotus japonicus young plants (two-week old)"
                     /dev_stage="young plants (two-week old)"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI; isolate=Miyakojima MG-20"
BASE COUNT      106 a     85 c    107 g     81 t
ORIGIN


  Query Match            90.6%;  Score 15.4;  DB 9;  Length 379;
  Best Local Similarity  94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    300 CGGGGTCTTACCGTCTT 284


RESULT 12
AI932079/c
LOCUS       AI932079                385 bp    mRNA    linear   EST 20-MAR-2000
DEFINITION  JAA000221.SH3 Adult SjC 7/94 Schistosoma japonicum cDNA 5', mRNA
            sequence.
ACCESSION   AI932079
VERSION     AI932079.1  GI:5670793
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 385)
  AUTHORS   Hu,W., Brindley,P.J. and Feng,Z.
  TITLE     Expressed sequence tags from adults of Schistosoma japonicum (Anhui
            strain) (Hu, Brindley, Feng)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Brindley, P.J.
            Molecular Parasitology Unit
            Queensland Institute of Medical Research
            300 Herston Road, Qeensland 4029, Australia
            Tel: 61 7 3362 0413
            Fax: 61 7 3362 0104
            Email: paulB@qimr.edu.au
            PCR PRimers
            FORWARD: M13 Forward
            BACKWARD: M13 Reverse
            Insert Length: 800   Std Error: 0.00
            Seq primer: T3 Reverse
            High quality sequence stop: 385.
FEATURES             Location/Qualifiers
     source          1. .385
                     /organism="Schistosoma japonicum"
                     /strain="Chinese (Anhui) strain"
                     /db_xref="taxon:6182"
                     /clone_lib="Adult SjC 7/94"
                     /sex="Male and female"
                     /tissue_type="Whole body"
                     /dev_stage="Adult worms"
                     /lab_host="Mouse and rabbit"
                     /note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
                     XhoI I; Several hundred adult Schistosoma japonicum (Anhui
                     , P.R. China, strain), of mixed sex, were perfused from
                     the mesenteries of experimentally infected mice and
                     rabbits at the Queensland Institute of Medical Research,
                     Brisbane, Australia (QIMR), and stored for several months
                     in liquid nitrogen. Subsequently, mRNA was isolated at the
                     QIMR from lysates of these worms by oligo dT
                     chromatography, using a kit from Pharmacia. The mRNA was
                     then shipped to Clontech, Palo Alto, CA, USA, who
                     constructed a cDNA library. First strand synthesis was
                     primed with an oligo-dT-XhoI-primer and synthesized using
                     M-MLV reverse transcriptase. Second strand synthesis was
                     accomplished with RNAse H and T4 DNA polymerase. The
                     double stranded cDNA was ligated to EcoRI linkers,
                     digested with EcoRI and XhoI, and ligated into the
                     phagemid vector lambda ZAP II XR. After construction of
                     this directional library by Clontech, it was returned to
                     the QIMR. During analysis of the library at the QIMR, we
                     have found that a small percentage, 2% to 3%, of the
                     clones contain inserts that appear to be highly homologous
                     to sequences from salmonoid fishes, as determined by
                     homology comparisons using BLAST and by Southern
                     hybridization analysis to genomic DNA from salmon (Sigma
                     Chemical Co., St. Louis, MO) under stringent washing
                     conditions. The remainder of the clones appear to contain
                     S. japonicum sequences."
BASE COUNT      112 a     47 c     74 g    152 t
ORIGIN


  Query Match            90.6%;  Score 15.4;  DB 9;  Length 385;
  Best Local Similarity  94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    358 CGGGGTCTTTCCGTCTT 342


RESULT 13
BI119300
LOCUS       BI119300                386 bp    mRNA    linear   EST 01-SEP-2001
DEFINITION  AR026H02PBC30IH02S Porcine Peripheral Blood Cell cDNA library, Cot
            30 Sus scrofa cDNA, mRNA sequence.
ACCESSION   BI119300
VERSION     BI119300.1  GI:15413410
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Rink,A., Santschi,E.M. and Beattie,C.W.
  TITLE     Amplified, Normalized cDNA Libraries from a Porcine Model of
            Orthopedic Implant Associated Staphylococcus aureus Infection
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Rink A
            Department of Animal Biotechnology
            College of Agriculture, Biotechnology and Natural Resources,
            University of Nevada, Reno
            MS 202, FA 103, 1664 N Virginia St, Reno, NV 89557-0236, USA
            Tel: 775 784 1705
            Fax: 775 784 1375
            Email: arink@cabnr.unr.edu
```

Tissues and cells are derived from a porcine model for implant-associated infection using 1000 cfu of Staphylococcus aureus in a tibial transection, reduced and internally fixed with a dynamic compression plate. NOTE: The sequences contain a 'cDNA adapter' etween the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCACGAG'.

```
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Sus scrofa"
                     /strain="crossbreed"
                     /db_xref="taxon:9823"
                     /clone_lib="Porcine Peripheral Blood Cell cDNA library,
                     Cot 30"
                     /tissue_type="Peripheral Blood Cell"
                     /cell_type="mixed"
                     /dev_stage="control, 5 month old castrated male"
                     /lab_host="SOLR"
                     /note="Vector: pBSK; Site_1: Eco RI; Site_2: XhoI; Tissues
                     and cells are derived from a porcine model for
                     implant-associated infection using 1000 cfu of
                     Staphylococcus aureus in a tibial transecti n, reduced and
                     internally fixed with a dynamic compression plate. NOTE:
                     The sequences contain a 'cDNA adapter' between the EcoRI
                     site and the start of the EST. The adapter sequence is
                     'AATTCGGCACGAG'."
BASE COUNT       53 a    112 c    144 g     67 t     10 others
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 10;  Length 386;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtctt 17
           |||||||||| ||||||
Db     194 CGGGGTCTTCTCGTCTT 210


RESULT  14
AV412952/c
LOCUS       AV412952                 398 bp    mRNA    linear   EST 23-MAY-2000
DEFINITION  AV412952 Lotus japonicus young plants (two-week old) Lotus
            japonicus cDNA clone MWM226e10_r 5', mRNA sequence.
ACCESSION   AV412952
VERSION     AV412952.1  GI:7742128
KEYWORDS    EST.
SOURCE      Lotus japonicus.
  ORGANISM  Lotus japonicus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
            Lotus.
REFERENCE   1  (bases 1 to 398)
  AUTHORS   Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  TITLE     Generation of 7137 non-redundant expressed sequence tags from a
            legume, Lotus japonicus
  JOURNAL   DNA Res. 7 (2), 127-130 (2000)
  MEDLINE   20277479
COMMENT     Contact: Yasukazu Nakamura
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .398
                     /organism="Lotus japonicus"
                     /db_xref="taxon:34305"
                     /clone="MWM226e10_r"
                     /clone_lib="Lotus japonicus young plants (two-week old)"
                     /dev_stage="young plants (two-week old)"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI; isolate=Miyakojima MG-20"
BASE COUNT      110 a     96 c    110 g     82 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 9;  Length 398;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtctt 17
           |||||||||| ||||||
Db     258 CGGGGTCTTACCGTCTT 242


RESULT  15
AI168886/c
LOCUS       AI168886                 399 bp    mRNA    linear   EST 05-OCT-1998
DEFINITION  JA00A031.QA3 Adult SjC 7/94 Schistosoma japonicum cDNA clone
            SJADA31 5' similar to Ribosomal RNA (mt), mRNA sequence.
ACCESSION   AI168886
VERSION     AI168886.1  GI:3702056
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 399)
  AUTHORS   Brindley,P.J. and Fan,J.
  TITLE     ESTs from Adults of Schistosoma japonicum (Anhui strain)
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Brindley, P.J.
            Molecular Parasitology Unit
            Queensland Institute of Medical Research
            300 Herston Road, Qeensland 4029, Australia
            Tel: 61 7 3362 0413
            Fax: 61 7 3362 0104
            Email: paulB@qimr.edu.au
            PCR PRimers
            FORWARD: M13 Forward
            BACKWARD: M13 Reverse
            Insert Length: 700   Std Error: 0.00
            Seq primer: T3 Reverse
            High quality sequence stop: 399.
FEATURES             Location/Qualifiers
     source          1. .399
                     /organism="Schistosoma japonicum"
                     /strain="Chinese (Anhui) strain"
                     /db_xref="taxon:6182"
                     /clone="SJADA31"
                     /clone_lib="Adult SjC 7/94"
                     /sex="Male and female"
                     /tissue_type="Whole body"
                     /dev_stage="Adult worms"
                     /lab_host="Mouse and rabbit"
                     /note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
                     Xhol I; Several hundred adult Schistosoma japonicum (Anhui
                     , P.R. China, strain), of mixed sex, were perfused from
                     the mesenteries of experimentally infected mice and
                     rabbits at the Queensland Institute of Medical Research,
                     Brisbane, Australia (QIMR), and stored for several months
                     in liquid nitrogen. Subsequently, mRNA was isolated at the
                     QIMR from lysates of these worms by oligo dT
                     chromatography, using a kit from Pharmacia. The mRNA was
                     then shipped to Clontech, Palo Alto, CA, USA, who
                     constructed a cDNA library. First strand synthesis was
                     primed with an oligo-dT-XhoI-primer and synthesized using
                     M-MLV reverse transcriptase. Second strand synthesis was
                     accomplished with RNAse H and T4 DNA polymerase. The
                     double stranded cDNA was ligated to EcoRI linkers,
                     digested with EcoRI and XhoI, and ligated into the
                     phagemid vector lambda ZAP II XR. After construction of
                     this directional library by Clontech, it was returned to
                     the QIMR. During analysis of the library at the QIMR, we
                     have found that a small percentage, 2% to 3%, of the
                     clones contain inserts that appear to be highly homologous
```

to sequences from salmonoid fishes, as determined by homology comparisons using BLAST and by Southern hybridization analysis to genomic DNA from salmon (Sigma Chemical Co., St. Louis, MO) under stringent washing conditions. The remainder of the clones appear to contain S. japonicum sequences."
BASE COUNT 123 a 44 c 81 g 151 t
ORIGIN

Query Match 90.6%; Score 15.4; DB 9; Length 399;
Best Local Similarity 94.1%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||| |||||||
Db 168 CGGGGTCTTTCCGTCTT 152

RESULT 16
AV416711/c
LOCUS AV416711 401 bp mRNA linear EST 23-MAY-2000
DEFINITION AV416711 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWM131a06_r 5', mRNA sequence.
ACCESSION AV416711
VERSION AV416711.1 GI:7745890
KEYWORDS EST.
SOURCE Lotus japonicus.
ORGANISM Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
REFERENCE 1 (bases 1 to 401)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
JOURNAL DNA Res. 7 (2), 127-130 (2000)
MEDLINE 20277479
COMMENT Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES Location/Qualifiers
source 1. .401
/organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone="MWM131a06_r"
/clone_lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI; isolate=Miyakojima MG-20"
BASE COUNT 113 a 91 c 113 g 84 t
ORIGIN

Query Match 90.6%; Score 15.4; DB 9; Length 401;
Best Local Similarity 94.1%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||| |||||||
Db 314 CGGGGTCTTACCGTCTT 298

RESULT 17
AI168905/c
LOCUS AI168905 413 bp mRNA linear EST 07-OCT-1998
DEFINITION JA00A150.QA3 Adult SjC 7/94 Schistosoma japonicum cDNA clone SJADA150 5' similar to Ribosomal RNA (mt), mRNA sequence.
ACCESSION AI168905
VERSION AI168905.1 GI:3705213
KEYWORDS EST.
SOURCE Schistosoma japonicum.
ORGANISM Schistosoma japonicum
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 413)
AUTHORS Brindley,P.J. and Fan,J.
TITLE ESTs from Adults of Schistosoma japonicum (Anhui strain)
JOURNAL Unpublished (1997)
COMMENT Contact: Brindley, P.J.
Molecular Parasitology Unit
Queensland Institute of Medical Research
300 Herston Road, Qeensland 4029, Australia
Tel: 61 7 3362 0413
Fax: 61 7 3362 0104
Email: paulB@qimr.edu.au
PCR PRimers
FORWARD: M13 Forward
BACKWARD: M13 Reverse
Insert Length: 900 Std Error: 0.00
Seq primer: T3 Reverse
High quality sequence stop: 413.
FEATURES Location/Qualifiers
source 1. .413
/organism="Schistosoma japonicum"
/strain="Chinese (Anhui) strain"
/db_xref="taxon:6182"
/clone="SJADA150"
/clone_lib="Adult SjC 7/94"
/sex="Male and female"
/tissue_type="Whole body"
/dev_stage="Adult worms"
/lab_host="Mouse and rabbit"
/note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2: Xhol I; Several hundred adult Schistosoma japonicum (Anhui , P.R. China, strain), of mixed sex, were perfused from the mesenteries of experimentally infected mice and rabbits at the Queensland Institute of Medical Research, Brisbane, Australia (QIMR), and stored for several months in liquid nitrogen. Subsequently, mRNA was isolated at the QIMR from lysates of these worms by oligo dT chromatography, using a kit from Pharmacia. The mRNA was then shipped to Clontech, Palo Alto, CA, USA, who constructed a cDNA library. First strand synthesis was primed with an oligo-dT-XhoI-primer and synthesized using M-MLV reverse transcriptase. Second strand synthesis was accomplished with RNAse H and T4 DNA polymerase. The double stranded cDNA was ligated to EcoRI linkers, digested with EcoRI and XhoI, and ligated into the phagemid vector lambda ZAP II XR. After construction of this directional library by Clontech, it was returned to the QIMR. During analysis of the library at the QIMR, we have found that a small percentage, 2% to 3%, of the clones contain inserts that appear to be highly homologous to sequences from salmonoid fishes, as determined by homology comparisons using BLAST and by Southern hybridization analysis to genomic DNA from salmon (Sigma Chemical Co., St. Louis, MO) under stringent washing conditions. The remainder of the clones appear to contain S. japonicum sequences."
BASE COUNT 126 a 49 c 86 g 147 t 5 others
ORIGIN

Query Match 90.6%; Score 15.4; DB 9; Length 413;
Best Local Similarity 94.1%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||| |||||||
Db 77 CGGGGTCTTTCCGTCTT 61

```
RESULT 18
AV414502/c
LOCUS       AV414502                414 bp    mRNA    linear   EST 23-MAY-2000
DEFINITION  AV414502 Lotus japonicus young plants (two-week old) Lotus
            japonicus cDNA clone MWM245a05_r 5', mRNA sequence.
ACCESSION   AV414502
VERSION     AV414502.1  GI:7743678
KEYWORDS    EST.
SOURCE      Lotus japonicus.
  ORGANISM  Lotus japonicus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
            Lotus.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  TITLE     Generation of 7137 non-redundant expressed sequence tags from a
            legume, Lotus japonicus
  JOURNAL   DNA Res. 7 (2), 127-130 (2000)
  MEDLINE   20277479
COMMENT     Contact: Yasukazu Nakamura
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .414
                     /organism="Lotus japonicus"
                     /db_xref="taxon:34305"
                     /clone="MWM245a05_r"
                     /clone_lib="Lotus japonicus young plants (two-week old)"
                     /dev_stage="young plants (two-week old)"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI; isolate=Miyakojima MG-20"
BASE COUNT      112 a     99 c    120 g     83 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 9;  Length 414;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    258 CGGGGTCTTACCGTCTT 242


RESULT 19
AI168891/c
LOCUS       AI168891                418 bp    mRNA    linear   EST 05-OCT-1998
DEFINITION  JA00A137.QA3 Adult SjC 7/94 Schistosoma japonicum cDNA clone
            SJADA137 5' similar to Subunit mitochondrial ribosomal RNA, mRNA
            sequence.
ACCESSION   AI168891
VERSION     AI168891.1  GI:3702061
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 418)
  AUTHORS   Brindley,P.J. and Fan,J.
  TITLE     ESTs from Adults of Schistosoma japonicum (Anhui strain)
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Brindley, P.J.
            Molecular Parasitology Unit
            Queensland Institute of Medical Research
            300 Herston Road, Qeensland 4029, Australia
            Tel: 61 7 3362 0413
            Fax: 61 7 3362 0104
            Email: paulB@qimr.edu.au
            PCR PRimers
            FORWARD: M13 Forward
            BACKWARD: M13 Reverse
            Insert Length: 1300   Std Error: 0.00
            Seq primer: T3 Reverse
            High quality sequence stop: 418.
FEATURES             Location/Qualifiers
     source          1. .418
                     /organism="Schistosoma japonicum"
                     /strain="Chinese (Anhui) strain"
                     /db_xref="taxon:6182"
                     /clone="SJADA137"
                     /clone_lib="Adult SjC 7/94"
                     /sex="Male and female"
                     /tissue_type="Whole body"
                     /dev_stage="Adult worms"
                     /lab_host="Mouse and rabbit"
                     /note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
                     Xhol I; Several hundred adult Schistosoma japonicum (Anhui
                     , P.R. China, strain), of mixed sex, were perfused from
                     the mesenteries of experimentally infected mice and
                     rabbits at the Queensland Institute of Medical Research,
                     Brisbane, Australia (QIMR), and stored for several months
                     in liquid nitrogen. Subsequently, mRNA was isolated at the
                     QIMR from lysates of these worms by oligo dT
                     chromatography, using a kit from Pharmacia. The mRNA was
                     then shipped to Clontech, Palo Alto, CA, USA, who
                     constructed a cDNA library. First strand synthesis was
                     primed with an oligo-dT-XhoI-primer and synthesized using
                     M-MLV reverse transcriptase. Second strand synthesis was
                     accomplished with RNAse H and T4 DNA polymerase. The
                     double stranded cDNA was ligated to EcoRI linkers,
                     digested with EcoRI and XhoI, and ligated into the
                     phagemid vector lambda ZAP II XR. After construction of
                     this directional library by Clontech, it was returned to
                     the QIMR. During analysis of the library at the QIMR, we
                     have found that a small percentage, 2% to 3%, of the
                     clones contain inserts that appear to be highly homologous
                     to sequences from salmonid fishes, as determined by
                     homology comparisons using BLAST and by Southern
                     hybridization analysis to genomic DNA from salmon (Sigma
                     Chemical Co., St. Louis, MO) under stringent washing
                     conditions. The remainder of the clones appear to contain
                     S. japonicum sequences."
BASE COUNT      121 a     42 c     75 g    180 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 9;  Length 418;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    365 CGGGGTCTTTCCGTCTT 349


RESULT 20
AI168893/c
LOCUS       AI168893                419 bp    mRNA    linear   EST 05-OCT-1998
DEFINITION  JA00A154.QA3 Adult SjC 7/94 Schistosoma japonicum cDNA clone
            SJADA154 5' similar to Large subunit mitochondrial rRNA, mRNA
            sequence.
ACCESSION   AI168893
VERSION     AI168893.1  GI:3702063
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 419)
  AUTHORS   Brindley,P.J. and Fan,J.
  TITLE     ESTs from Adults of Schistosoma japonicum (Anhui strain)
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Brindley, P.J.
```

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Queensland Institute of Medical Research
300 Herston Road, Qeensland 4029, Australia
Tel: 61 7 3362 0413
Fax: 61 7 3362 0104
Email: paulB@qimr.edu.au
PCR PRimers
FORWARD: M13 Forward
BACKWARD: M13 Reverse
Insert Length: 1000 Std Error: 0.00
Seq primer: T3 Reverse
High quality sequence stop: 419.

FEATURES Location/Qualifiers
source 1. .419
/organism="Schistosoma japonicum"
/strain="Chinese (Anhui) strain"
/db_xref="taxon:6182"
/clone="SJADA154"
/clone_lib="Adult SjC 7/94"
/sex="Male and female"
/tissue_type="Whole body"
/dev_stage="Adult worms"
/lab_host="Mouse and rabbit"
/note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2: Xhol I; Several hundred adult Schistosoma japonicum (Anhui , P.R. China, strain), of mixed sex, were perfused from the mesenteries of experimentally infected mice and rabbits at the Queensland Institute of Medical Research, Brisbane, Australia (QIMR), and stored for several months in liquid nitrogen. Subsequently, mRNA was isolated at the QIMR from lysates of these worms by oligo dT chromatography, using a kit from Pharmacia. The mRNA was then shipped to Clontech, Palo Alto, CA, USA, who constructed a cDNA library. First strand synthesis was primed with an oligo-dT-XhoI-primer and synthesized using M-MLV reverse transcriptase. Second strand synthesis was accomplished with RNAse H and T4 DNA polymerase. The double stranded cDNA was ligated to EcoRI linkers, digested with EcoRI and XhoI, and ligated into the phagemid vector lambda ZAP II XR. After construction of this directional library by Clontech, it was returned to the QIMR. During analysis of the library at the QIMR, we have found that a small percentage, 2% to 3%, of the clones contain inserts that appear to be highly homologous to sequences from salmonoid fishes, as determined by homology comparisons using BLAST and by Southern hybridization analysis to genomic DNA from salmon (Sigma Chemical Co., St. Louis, MO) under stringent washing conditions. The remainder of the clones appear to contain S. japonicum sequences."

BASE COUNT 122 a 46 c 79 g 169 t 3 others
ORIGIN

Query Match 90.6%; Score 15.4; DB 9; Length 419;
Best Local Similarity 94.1%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||| |||||||
Db 388 CGGGGTCTTTCCGTCTT 372

RESULT 21
AV428402/c
LOCUS AV428402 421 bp mRNA linear EST 23-MAY-2000
DEFINITION AV428402 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWM096d03_r 5', mRNA sequence.
ACCESSION AV428402
VERSION AV428402.1 GI:7789321
KEYWORDS EST.
SOURCE Lotus japonicus.
ORGANISM Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
REFERENCE 1 (bases 1 to 421)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
JOURNAL DNA Res. 7 (2), 127-130 (2000)
MEDLINE 20277479
COMMENT Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES Location/Qualifiers
source 1. .421
/organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone="MWM096d03_r"
/clone_lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI; isolate=Miyakojima MG-20"
BASE COUNT 118 a 98 c 116 g 89 t
ORIGIN

Query Match 90.6%; Score 15.4; DB 9; Length 421;
Best Local Similarity 94.1%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||| |||||||
Db 398 CGGGGTCTTACCGTCTT 382

RESULT 22
AV426304/c
LOCUS AV426304 425 bp mRNA linear EST 23-MAY-2000
DEFINITION AV426304 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWM065e08_r 5', mRNA sequence.
ACCESSION AV426304
VERSION AV426304.1 GI:7785105
KEYWORDS EST.
SOURCE Lotus japonicus.
ORGANISM Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
REFERENCE 1 (bases 1 to 425)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
JOURNAL DNA Res. 7 (2), 127-130 (2000)
MEDLINE 20277479
COMMENT Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES Location/Qualifiers
source 1. .425
/organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone="MWM065e08_r"
/clone_lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI; isolate=Miyakojima MG-20"
BASE COUNT 120 a 100 c 114 g 91 t
ORIGIN

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  Query Match             90.6%;  Score 15.4;  DB 9;  Length 425;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    285 CGGGGTCTTACCGTCTT 269


RESULT  23
AW707310/c
LOCUS       AW707310                427 bp    mRNA    linear   EST 18-APR-2000
DEFINITION  JAA000647.SH3 Adult SjC 7/94 Schistosoma japonicum cDNA 5', mRNA
            sequence.
ACCESSION   AW707310
VERSION     AW707310.1  GI:7591580
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 427)
  AUTHORS   Hu,W., Brindley,P.J. and Feng,Z.
  TITLE     Expressed sequence tags from adults of Schistosoma japonicum (Anhui
            strain) (Hu, Brindley, Feng)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Brindley, P.J.
            Molecular Parasitology Unit
            Queensland Institute of Medical Research
            300 Herston Road, Qeensland 4029, Australia
            Tel: 61 7 3362 0413
            Fax: 61 7 3362 0104
            Email: paulB@qimr.edu.au
            PCR PRimers
            FORWARD: M13 Forward
            BACKWARD: M13 Reverse
            Insert Length: 1000   Std Error: 0.00
            Seq primer: T3 Reverse
            High quality sequence stop: 427.
FEATURES             Location/Qualifiers
     source          1. .427
                     /organism="Schistosoma japonicum"
                     /strain="Chinese (Anhui) strain"
                     /db_xref="taxon:6182"
                     /clone_lib="Adult SjC 7/94"
                     /sex="Male and female"
                     /tissue_type="Whole body"
                     /dev_stage="Adult worms"
                     /lab_host="Mouse and rabbit"
                     /note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
                     Xhol I; Several hundred adult Schistosoma japonicum (Anhui
                     , P.R. China, strain), of mixed sex, were perfused from
                     the mesenteries of experimentally infected mice and
                     rabbits at the Queensland Institute of Medical Research,
                     Brisbane, Australia (QIMR), and stored for several months
                     in liquid nitrogen. Subsequently, mRNA was isolated at the
                     QIMR from lysates of these worms by oligo dT
                     chromatography, using a kit from Pharmacia. The mRNA was
                     then shipped to Clontech, Palo Alto, CA, USA, who
                     constructed a cDNA library. First strand synthesis was
                     primed with an oligo-dT-XhoI-primer and synthesized using
                     M-MLV reverse transcriptase. Second strand synthesis was
                     accomplished with RNAse H and T4 DNA polymerase. The
                     double stranded cDNA was ligated to EcoRI linkers,
                     digested with EcoRI and XhoI, and ligated into the
                     phagemid vector lambda ZAP II XR. After construction of
                     this directional library by Clontech, it was returned to
                     the QIMR. During analysis of the library at the QIMR, we
                     have found that a small percentage, 2% to 3%, of the
                     clones contain inserts that appear to be highly homologous
                     to sequences from salmonoid fishes, as determined by
                     homology comparisons using BLAST and by Southern
                     hybridization analysis to genomic DNA from salmon (Sigma
                     Chemical Co., St. Louis, MO) under stringent washing
                     conditions. The remainder of the clones appear to contain
                     S. japonicum sequences."
BASE COUNT      124 a     44 c     75 g    184 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 9;  Length 427;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    361 CGGGGTCTTTCCGTCTT 345


RESULT  24
AW736775/c
LOCUS       AW736775                433 bp    mRNA    linear   EST 25-APR-2000
DEFINITION  JAYL0254.GYL Schistosoma japonicum Lambda gt11 Express library
            Schistosoma japonicum cDNA clone JAYL0254.GY 5', mRNA sequence.
ACCESSION   AW736775
VERSION     AW736775.1  GI:7644639
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 433)
  AUTHORS   Li,Y., Wu,Z.D. and Yu,X.B.
  TITLE     Expressed sequence tags from adults of Schistosoma japonicum
            (Chinese strain) (Li,Y.; Wu,Z.D.; Yu,X.B.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Wu ZD
            Department of Parasitology
            Sun-Yat-sen University of Medical Sciences
            BOX 510089, 74# Zhongshen Er Road,Gaungzhou, Guangdong, P.R.China
            Tel: 86-20-87330566
            Fax: 86-20- 87331679
            Email: zdwu62@163.net
            PCR PRimers
            FORWARD: Lambda gt11 Forward Primer
            BACKWARD: Lambda gt11 Reverse Primer
            Seq primer: Lambda gt11 Forward Primer
            High quality sequence stop: 433.
FEATURES             Location/Qualifiers
     source          1. .433
                     /organism="Schistosoma japonicum"
                     /strain="Chinese"
                     /db_xref="taxon:6182"
                     /clone="JAYL0254.GY"
                     /clone_lib="Schistosoma japonicum Lambda gt11 Express
                     library"
                     /sex="Mix"
                     /note="Vector: Lambda gt11 Sfi-Not; Site_1: EcoRI; Site_2:
                     NotI; Several hundred adult Schistosoma japonicum(Jiangxi,
                     P.R.China, strain),  of mixed sex, were perfused from the
                     mesenteries of experimentally  infected rabbits.
                     Double-strain cDNA synthesized with the mRNA  isolated
                     from adult worm, was inserted into the bacteriophage
                     lambda  gt11 Sfi-Not arms between EcoRI and NotI site of
                     the LacZ gene. The cDNA library was contructed by Chen
                     S.Z. at Nanjing Medical  University, Nanjing, Jiangsu,
                     P.R. China. (see:  Chen Shuzhen, et al. Chinese Journal of
                     Zoonoses 1997,13(6): 23-25)"
BASE COUNT      145 a     46 c     91 g    151 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 9;  Length 433;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
```

```
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db     81 CGGGGTCTTTCCGTCTT 65


RESULT  25
BF327832/c
LOCUS       BF327832                437 bp    mRNA    linear   EST 22-NOV-2000
DEFINITION  PM0-BN0144-160600-004-e08 BN0144 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF327832
VERSION     BF327832.1  GI:11298580
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 437)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM0&t2=PM0-BN0144-
            160600-004-e08&t3=2000-06-16&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 25
            High quality sequence stop: 437.
FEATURES             Location/Qualifiers
     source          1. .437
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="BN0144"
                     /dev_stage="Adult"
                     /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT      126 a    120 c    113 g     78 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 10;  Length 437;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          |||||||||| |||||
Db    429 CGGGGTCTTCCTGTCTT 413


RESULT  26
BG810759
LOCUS       BG810759                439 bp    mRNA    linear   EST 22-MAY-2001
DEFINITION  daf30h02.x1 NICHD XGC Brn1 Xenopus laevis cDNA clone IMAGE:4740314
            3', mRNA sequence.
ACCESSION   BG810759
VERSION     BG810759.1  GI:14181739
KEYWORDS    EST.
SOURCE      African clawed frog.
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 439)
  AUTHORS   Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.
            , Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
            ,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Xenopus EST project, 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Sandy Clifton, Ph.D.
            WashU Xenopus EST project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: Xenopus clones from this library are available
            through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
            High quality sequence stop: 416.
FEATURES             Location/Qualifiers
     source          1. .439
                     /organism="Xenopus laevis"
                     /db_xref="taxon:8355"
                     /clone="IMAGE:4740314"
                     /clone_lib="NICHD XGC Brn1"
                     /dev_stage="adult"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.5 kb. Constructed by Life
                     Technologies. Note: This is a Xenopus Gene Collection (XGC
                     ) library."
BASE COUNT      146 a    114 c     53 g    126 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 10;  Length 439;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    320 CGGGGTCTTTCCGTCTT 336


RESULT  27
AV423171/c
LOCUS       AV423171                442 bp    mRNA    linear   EST 23-MAY-2000
DEFINITION  AV423171 Lotus japonicus young plants (two-week old) Lotus
            japonicus cDNA clone MWM023h05_r 5', mRNA sequence.
ACCESSION   AV423171
VERSION     AV423171.1  GI:7778815
KEYWORDS    EST.
SOURCE      Lotus japonicus.
  ORGANISM  Lotus japonicus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
            Lotus.
REFERENCE   1  (bases 1 to 442)
  AUTHORS   Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  TITLE     Generation of 7137 non-redundant expressed sequence tags from a
```

```
          legume, Lotus japonicus
  JOURNAL   DNA Res. 7 (2), 127-130 (2000)
  MEDLINE   20277479
COMMENT     Contact: Yasukazu Nakamura
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .442
                     /organism="Lotus japonicus"
                     /db_xref="taxon:34305"
                     /clone="MWM023h05_r"
                     /clone_lib="Lotus japonicus young plants (two-week old)"
                     /dev_stage="young plants (two-week old)"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI; isolate=Miyakojima MG-20"
BASE COUNT      123 a    102 c    120 g     97 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 9;  Length 442;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    398 CGGGGTCTTACCGTCTT 382


RESULT  28
BE345961
LOCUS       BE345961                451 bp    mRNA    linear   EST 17-JUL-2000
DEFINITION  JAA000767.SH3 Adult SjC 7/94 Schistosoma japonicum cDNA 5', mRNA
            sequence.
ACCESSION   BE345961
VERSION     BE345961.1  GI:9255493
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 451)
  AUTHORS   Hu,W., Brindley,P.J. and Feng,Z.
  TITLE     Expressed sequence tags from adults of Schistosoma japonicum (Anhui
            strain) (Hu, Brindley, Feng)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Brindley, P.J.
            Molecular Parasitology Unit
            Queensland Institute of Medical Research
            300 Herston Road, Qeensland 4029, Australia
            Tel: 61 7 3362 0413
            Fax: 61 7 3362 0104
            Email: paulB@qimr.edu.au
            PCR PRimers
            FORWARD: M13 Forward
            BACKWARD: M13 Reverse
            Seq primer: T3 Reverse
            High quality sequence stop: 451.
FEATURES             Location/Qualifiers
     source          1. .451
                     /organism="Schistosoma japonicum"
                     /strain="Chinese (Anhui) strain"
                     /db_xref="taxon:6182"
                     /clone_lib="Adult SjC 7/94"
                     /sex="Male and female"
                     /tissue_type="Whole body"
                     /dev_stage="Adult worms"
                     /lab_host="Mouse and rabbit"
                     /note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
                     Xhol I; Several hundred adult Schistosoma japonicum (Anhui
                     , P.R. China, strain), of mixed sex, were perfused from
                     the mesenteries of experimentally infected mice and
                     rabbits at the Queensland Institute of Medical Research,
                     Brisbane, Australia (QIMR), and stored for several months
                     in liquid nitrogen. Subsequently, mRNA was isolated at the
                     QIMR from lysates of these worms by oligo dT
                     chromatography, using a kit from Pharmacia. The mRNA was
                     then shipped to Clontech, Palo Alto, CA, USA, who
                     constructed a cDNA library. First strand synthesis was
                     primed with an oligo-dT-XhoI-primer and synthesized using
                     M-MLV reverse transcriptase. Second strand synthesis was
                     accomplished with RNAse H and T4 DNA polymerase. The
                     double stranded cDNA was ligated to EcoRI linkers,
                     digested with EcoRI and XhoI, and ligated into the
                     phagemid vector lambda ZAP II XR. After construction of
                     this directional library by Clontech, it was returned to
                     the QIMR. During analysis of the library at the QIMR, we
                     have found that a small percentage, 2% to 3%, of the
                     clones contain inserts that appear to be highly homologous
                     to sequences from salmonoid fishes, as determined by
                     homology comparisons using BLAST and by Southern
                     hybridization analysis to genomic DNA from salmon (Sigma
                     Chemical Co., St. Louis, MO) under stringent washing
                     conditions. The remainder of the clones appear to contain
                     S. japonicum sequences."
BASE COUNT      157 a     92 c     55 g    147 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 10;  Length 451;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    373 CGGGGTCTTTCCGTCTT 389


RESULT  29
AW736765/c
LOCUS       AW736765                475 bp    mRNA    linear   EST 25-APR-2000
DEFINITION  JAYG00039.GYL Schistosoma japonicum Lambda gt11 Express library
            Schistosoma japonicum cDNA clone JAYG00039.GY 5', mRNA sequence.
ACCESSION   AW736765
VERSION     AW736765.1  GI:7644629
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 475)
  AUTHORS   Bian,G., Wu,Z.D. and Yu,X.B.
  TITLE     Expressed sequence tags from adults of Schistosoma japonicum
            (Chinese strain) (Bian,G.; Wu,Z.D.; Yu,X.B.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Wu ZD
            Department of Parasitology
            Sun-Yat-sen University of Medical Sciences
            BOX 510089, 74# Zhongshen Er Road,Gaungzhou, Guangdong, P.R.China
            Tel: 86-20-87330566
            Fax: 86-20- 87331679
            Email: zdwu62@163.net
            PCR PRimers
            FORWARD: Lambda gt11 Forward Primer
            BACKWARD: Lambda gt11 Reverse Primer
            Seq primer: Lambda gt11 Forward Primer
            High quality sequence stop: 475.
FEATURES             Location/Qualifiers
     source          1. .475
                     /organism="Schistosoma japonicum"
                     /strain="Chinese"
                     /db_xref="taxon:6182"
                     /clone="JAYG00039.GY"
                     /clone_lib="Schistosoma japonicum Lambda gt11 Express
                     library"
```

```
                     /sex="Mix"
                     /note="Vector: Lambda gt11 Sfi-Not; Site_1: EcoRI; Site_2:
                     NotI; Several hundred adult Schistosoma japonicum(Jiangxi,
                     P.R.China, strain), of mixed sex, were perfused from the
                     mesenteries of experimentally infected rabbits.
                     Double-strain cDNA synthesized with the mRNA isolated
                     from adult worm, was inserted into the bacteriophage
                     lambda gt11 Sfi-Not arms between EcoRI and NotI site of
                     the LacZ gene. The cDNA library was contructed by Chen
                     S.Z. at Nanjing Medical University, Nanjing, Jiangsu,
                     P.R. China. (see: Chen Shuzhen, et al. Chinese Journal of
                     Zoonoses 1997,13(6): 23-25)"
BASE COUNT      155 a     51 c     99 g    170 t
ORIGIN


  Query Match            90.6%;  Score 15.4;  DB 9;  Length 475;
  Best Local Similarity  94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    128 CGGGGTCTTTCCGTCTT 112


RESULT  30
BE819808/c
LOCUS       BE819808                483 bp    mRNA    linear   EST 21-SEP-2000
DEFINITION  JAYB0164.GYL Schistosoma japonicum Lambda gt11 Express library
            Schistosoma japonicum cDNA clone JAYB0164.GY 5', mRNA sequence.
ACCESSION   BE819808
VERSION     BE819808.1  GI:10252042
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 483)
  AUTHORS   Bian,G., Wu,Z.D. and Yu,X.B.
  TITLE     Expressed sequence tags from adults of Schistosoma japonicum
            (Chinese strain) (Bian,G.; Wu,Z.D.; Yu,X.B.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Wu ZD
            Department of Parasitology
            Sun-Yat-sen University of Medical Sciences
            BOX 510089, 74# Zhongshen Er Road,Gaungzhou, Guangdong, P.R.China
            Tel: 86-20-87330566
            Fax: 86-20- 87331679
            Email: zdwu62@163.net
            PCR PRimers
            FORWARD: Lambda gt11 Forward Primer
            BACKWARD: Lambda gt11 Reverse Primer
            Seq primer: Lambda gt11 Forward Primer
            High quality sequence stop: 483.
FEATURES             Location/Qualifiers
     source          1. .483
                     /organism="Schistosoma japonicum"
                     /strain="Chinese"
                     /db_xref="taxon:6182"
                     /clone="JAYB0164.GY"
                     /clone_lib="Schistosoma japonicum Lambda gt11 Express
                     library"
                     /sex="Mix"
                     /note="Vector: Lambda gt11 Sfi-Not; Site_1: EcoRI; Site_2:
                     NotI; Several hundred adult Schistosoma japonicum(Jiangxi,
                     P.R.China, strain), of mixed sex, were perfused from the
                     mesenteries of experimentally infected rabbits.
                     Double-strain cDNA synthesized with the mRNA isolated
                     from adult worm, was inserted into the bacteriophage
                     lambda gt11 Sfi-Not arms between EcoRI and NotI site of
                     the LacZ gene. The cDNA library was contructed by Chen
                     S.Z. at Nanjing Medical University, Nanjing, Jiangsu,
                     P.R. China. (see: Chen Shuzhen, et al. Chinese Journal of
                     Zoonoses 1997,13(6): 23-25)"
BASE COUNT      156 a     54 c    102 g    171 t
ORIGIN


  Query Match            90.6%;  Score 15.4;  DB 10;  Length 483;
  Best Local Similarity  94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    136 CGGGGTCTTTCCGTCTT 120


RESULT  31
AW707291/c
LOCUS       AW707291                484 bp    mRNA    linear   EST 18-APR-2000
DEFINITION  JAA000628.SH3 Adult SjC 7/94 Schistosoma japonicum cDNA 5', mRNA
            sequence.
ACCESSION   AW707291
VERSION     AW707291.1  GI:7591561
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 484)
  AUTHORS   Hu,W., Brindley,P.J. and Feng,Z.
  TITLE     Expressed sequence tags from adults of Schistosoma japonicum (Anhui
            strain) (Hu, Brindley, Feng)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Brindley, P.J.
            Molecular Parasitology Unit
            Queensland Institute of Medical Research
            300 Herston Road, Qeensland 4029, Australia
            Tel: 61 7 3362 0413
            Fax: 61 7 3362 0104
            Email: paulB@qimr.edu.au
            PCR PRimers
            FORWARD: M13 Forward
            BACKWARD: M13 Reverse
            Insert Length: 1000   Std Error: 0.00
            Seq primer: T3 Reverse
            High quality sequence stop: 484.
FEATURES             Location/Qualifiers
     source          1. .484
                     /organism="Schistosoma japonicum"
                     /strain="Chinese (Anhui) strain"
                     /db_xref="taxon:6182"
                     /clone_lib="Adult SjC 7/94"
                     /sex="Male and female"
                     /tissue_type="Whole body"
                     /dev_stage="Adult worms"
                     /lab_host="Mouse and rabbit"
                     /note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
                     Xhol I; Several hundred adult Schistosoma japonicum (Anhui
                     , P.R. China, strain), of mixed sex, were perfused from
                     the mesenteries of experimentally infected mice and
                     rabbits at the Queensland Institute of Medical Research,
                     Brisbane, Australia (QIMR), and stored for several months
                     in liquid nitrogen. Subsequently, mRNA was isolated at the
                     QIMR from lysates of these worms by oligo dT
                     chromatography, using a kit from Pharmacia. The mRNA was
                     then shipped to Clontech, Palo Alto, CA, USA, who
                     constructed a cDNA library. First strand synthesis was
                     primed with an oligo-dT-XhoI-primer and synthesized using
                     M-MLV reverse transcriptase. Second strand synthesis was
                     accomplished with RNAse H and T4 DNA polymerase. The
                     double stranded cDNA was ligated to EcoRI linkers,
                     digested with EcoRI and XhoI, and ligated into the
                     phagemid vector lambda ZAP II XR. After construction of
                     this directional library by Clontech, it was returned to
                     the QIMR. During analysis of the library at the QIMR, we
```

have found that a small percentage, 2% to 3%, of the clones contain inserts that appear to be highly homologous to sequences from salmonoid fishes, as determined by homology comparisons using BLAST and by Southern hybridization analysis to genomic DNA from salmon (Sigma Chemical Co., St. Louis, MO) under stringent washing conditions. The remainder of the clones appear to contain S. japonicum sequences."

BASE COUNT 144 a 54 c 106 g 180 t
ORIGIN

Query Match 90.6%; Score 15.4; DB 9; Length 484;
Best Local Similarity 94.1%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||| |||||||
Db 153 CGGGGTCTTTCCGTCTT 137

RESULT 32
AV428939/c
LOCUS AV428939 500 bp mRNA linear EST 02-MAY-2000
DEFINITION AV428939 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWM093d08_r 5', mRNA sequence.
ACCESSION AV428939
VERSION AV428939.1 GI:7678321
KEYWORDS EST.
SOURCE Lotus japonicus.
ORGANISM Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
REFERENCE 1 (bases 1 to 500)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
JOURNAL DNA Res. 7 (2), 127-130 (2000)
MEDLINE 20277479
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES Location/Qualifiers
source 1. .500
/organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone="MWM093d08_r"
/clone_lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI; isolate=Miyakojima MG-20"
BASE COUNT 135 a 113 c 151 g 101 t
ORIGIN

Query Match 90.6%; Score 15.4; DB 9; Length 500;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||| |||||||
Db 226 CGGGGTCTTACCGTCTT 210

RESULT 33
BE123840/c
LOCUS BE123840 505 bp mRNA linear EST 14-JUN-2000
DEFINITION JAYB0147.GYL Schistosoma japonicum Lambda gt11 Express library Schistosoma japonicum cDNA clone JAYB0147.GY 5', mRNA sequence.
ACCESSION BE123840
VERSION BE123840.1 GI:8517154
KEYWORDS EST.
SOURCE Schistosoma japonicum.
ORGANISM Schistosoma japonicum
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 505)
AUTHORS Bao,J., Wu,Z.D. and Yu,X.B.
TITLE Expressed sequence tags from adults of Schistosoma japonicum (Chinese strain) (Bao,J.; Wu,Z.D.; Yu,X.B.)
JOURNAL Unpublished (2000)
COMMENT Contact: Wu ZD
Department of Parasitology
Sun-Yat-sen University of Medical Sciences
BOX 510089, 74# Zhongshen Er Road,Gaungzhou, Guangdong, P.R.China
Tel: 86-20-87330566
Fax: 86-20- 87331679
Email: zdwu62@163.net
PCR PRimers
FORWARD: Lambda gt11 Forward Primer
BACKWARD: Lambda gt11 Reverse Primer
Seq primer: Lambda gt11 Forward Primer
High quality sequence stop: 505.
FEATURES Location/Qualifiers
source 1. .505
/organism="Schistosoma japonicum"
/strain="Chinese"
/db_xref="taxon:6182"
/clone="JAYB0147.GY"
/clone_lib="Schistosoma japonicum Lambda gt11 Express library"
/sex="Mix"
/note="Vector: Lambda gt11 Sfi-Not; Site_1: EcoRI; Site_2: NotI; Several hundred adult Schistosoma japonicum(Jiangxi, P.R.China, strain), of mixed sex, were perfused from the mesenteries of experimentally infected rabbits. Double-strain cDNA synthesized with the mRNA isolated from adult worm, was inserted into the bacteriophage lambda gt11 Sfi-Not arms between EcoRI and NotI site of the LacZ gene. The cDNA library was contructed by Chen S.Z. at Nanjing Medical University, Nanjing, Jiangsu, P.R. China. (see: Chen Shuzhen, et al. Chinese Journal of Zoonoses 1997,13(6): 23-25)"
BASE COUNT 167 a 54 c 106 g 178 t
ORIGIN

Query Match 90.6%; Score 15.4; DB 9; Length 505;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||| |||||||
Db 152 CGGGGTCTTTCCGTCTT 136

RESULT 34
BI403676
LOCUS BI403676 506 bp mRNA linear EST 14-AUG-2001
DEFINITION MI-P-CP1-nwk-d-10-0-UI.s1 MI-P-CP1 Sus scrofa cDNA clone MI-P-CP1-nwk-d-10-0-UI 3', mRNA sequence.
ACCESSION BI403676
VERSION BI403676.1 GI:15182737
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 506)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery

```
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Tuggle CK
            Molecular Genetics Laboratory, Department of Animal Science
            Iowa State University
            201 Kildee Hall, Ames, IA 50011-3150, USA
            Tel: 5152944252
            Fax: 5152942401
            Email: cktuggle@iastate.edu
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.B.
            Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab,
            University of Iowa Clone distribution: clones will be available
            through Research Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .506
                     /organism="Sus scrofa"
                     /strain="crossbreed"
                     /db_xref="taxon:9823"
                     /clone="MI-P-CP1-nwk-d-10-0-UI"
                     /clone_lib="MI-P-CP1"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-CP1
                     library is normalized library derived from the MI-P-CP0
                     library,  ultimately derived from uterus tissue. For a
                     detailed description of the  library from which this clone
                     was derived, please visit our web site at
                     http://pigest.genome.iastate.edu/. The procedure used to
                     create this library has been previously described (Bonaldo
                     , Lennon and Soares, Genome Research 6: 791-806, 1996)
                     TAG_SEQ=None found"
BASE COUNT       79 a    157 c    174 g     96 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 10;  Length 506;
  Best Local Similarity   94.1%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db    265 CGGGGTCTTCTCGTCTT 281


RESULT  35
AW786990
LOCUS       AW786990                512 bp    mRNA    linear   EST 09-JUL-2000
DEFINITION  120660 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   AW786990
VERSION     AW786990.1  GI:7843766
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 512)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 44  row: E  column: 13
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .512
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /clone_lib="MARC 1PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from day 11, 13, 15, 20,
                     and 30 embryos."
BASE COUNT       79 a    156 c    162 g    115 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 9;  Length 512;
  Best Local Similarity   94.1%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||||| ||||||
Db     81 CGGGGTCTTCTCGTCTT 97


RESULT  36
AU216075
LOCUS       AU216075                517 bp    mRNA    linear   EST 17-JUL-2001
DEFINITION  AU216075 unpublished oligo-capped cDNA library, stage L1
            Caenorhabditis elegans cDNA clone yk833e01 3', mRNA sequence.
ACCESSION   AU216075
VERSION     AU216075.1  GI:14854232
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans.
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
            ; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 517)
  AUTHORS   Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
            and Sugano,S.
  TITLE     A complementary view of the C.elegans genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yuji Kohara
            Genome Biology Lab.
            National Institute of Genetics
            Yata 1111, Mishima, Shizuoka 411, Japan
            Tel: 81-559-81-6854
            Fax: 81-559-81-6855
            Email: ykohara@lab.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .517
                     /organism="Caenorhabditis elegans"
                     /strain="N2"
                     /db_xref="taxon:6239"
                     /clone="yk833e01"
                     /clone_lib="unpublished oligo-capped cDNA library, stage
                     L1"
                     /sex="Hermaphrodite"
                     /tissue_type="whole animal"
                     /dev_stage="L1"
BASE COUNT      116 a     91 c    150 g    160 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 9;  Length 517;
  Best Local Similarity   94.1%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
```

```
          ||||||||||| |||||
Db    205 CGGGGTCTTCCAGTCTT 221


RESULT 37
AI932095/c
LOCUS       AI932095                523 bp    mRNA    linear   EST 20-MAR-2000
DEFINITION  JAA000237.SH3 Adult SjC 7/94 Schistosoma japonicum cDNA 5', mRNA
            sequence.
ACCESSION   AI932095
VERSION     AI932095.1  GI:5670809
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 523)
  AUTHORS   Hu,W., Brindley,P.J. and Feng,Z.
  TITLE     Expressed sequence tags from adults of Schistosoma japonicum (Anhui
            strain) (Hu, Brindley, Feng)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Brindley, P.J.
            Molecular Parasitology Unit
            Queensland Institute of Medical Research
            300 Herston Road, Qeensland 4029, Australia
            Tel: 61 7 3362 0413
            Fax: 61 7 3362 0104
            Email: paulB@qimr.edu.au
            PCR PRimers
            FORWARD: M13 Forward
            BACKWARD: M13 Reverse
            Insert Length: 700   Std Error: 0.00
            Seq primer: T3 Reverse
            High quality sequence stop: 523.
FEATURES             Location/Qualifiers
     source          1. .523
                     /organism="Schistosoma japonicum"
                     /strain="Chinese (Anhui) strain"
                     /db_xref="taxon:6182"
                     /clone_lib="Adult SjC 7/94"
                     /sex="Male and female"
                     /tissue_type="Whole body"
                     /dev_stage="Adult worms"
                     /lab_host="Mouse and rabbit"
                     /note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
                     XhoI I; Several hundred adult Schistosoma japonicum (Anhui
                     , P.R. China, strain), of mixed sex, were perfused from
                     the mesenteries of experimentally infected mice and
                     rabbits at the Queensland Institute of Medical Research,
                     Brisbane, Australia (QIMR), and stored for several months
                     in liquid nitrogen. Subsequently, mRNA was isolated at the
                     QIMR from lysates of these worms by oligo dT
                     chromatography, using a kit from Pharmacia. The mRNA was
                     then shipped to Clontech, Palo Alto, CA, USA, who
                     constructed a cDNA library. First strand synthesis was
                     primed with an oligo-dT-XhoI-primer and synthesized using
                     M-MLV reverse transcriptase. Second strand synthesis was
                     accomplished with RNAse H and T4 DNA polymerase. The
                     double stranded cDNA was ligated to EcoRI linkers,
                     digested with EcoRI and XhoI, and ligated into the
                     phagemid vector lambda ZAP II XR. After construction of
                     this directional library by Clontech, it was returned to
                     the QIMR. During analysis of the library at the QIMR, we
                     have found that a small percentage, 2% to 3%, of the
                     clones contain inserts that appear to be highly homologous
                     to sequences from salmonoid fishes, as determined by
                     homology comparisons using BLAST and by Southern
                     hybridization analysis to genomic DNA from salmon (Sigma
                     Chemical Co., St. Louis, MO) under stringent washing
                     conditions. The remainder of the clones appear to contain
                     S. japonicum sequences."
BASE COUNT      157 a     60 c    115 g    191 t
ORIGIN
```

```
  Query Match            90.6%;  Score 15.4;  DB 9;  Length 523;
  Best Local Similarity  94.1%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    192 CGGGGTCTTTCCGTCTT 176


RESULT 38
AW329878/c
LOCUS       AW329878                554 bp    mRNA    linear   EST 28-JAN-2000
DEFINITION  JAYL0232.GYL Schistosoma japonicum Lambda gt11 Express library
            Schistosoma japonicum cDNA clone JAYL0232.GY 5', mRNA sequence.
ACCESSION   AW329878
VERSION     AW329878.1  GI:6806936
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 554)
  AUTHORS   Li,Y., Wu,Z.D. and Yu,X.B.
  TITLE     Expressed sequence tags from adults of Schistosoma japonicum
            (Chinese strain) (Li,Y.; Wu,Z.D.; Yu,X.B.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Wu ZD
            Department of Parasitology
            Sun-Yat-sen University of Medical Sciences
            BOX 510089, 74# Zhongshen Er Road,Gaungzhou, Guangdong, P.R.China
            Tel: 86-20-87330566
            Fax: 86-20- 87331679
            Email: zdwu62@163.net
            PCR PRimers
            FORWARD: Lambda gt11 Forward Primer
            BACKWARD: Lambda gt11 Reverse Primer
            Seq primer: Lambda gt11 Forward Primer
            High quality sequence stop: 554.
FEATURES             Location/Qualifiers
     source          1. .554
                     /organism="Schistosoma japonicum"
                     /strain="Chinese"
                     /db_xref="taxon:6182"
                     /clone="JAYL0232.GY"
                     /clone_lib="Schistosoma japonicum Lambda gt11 Express
                     library"
                     /sex="Mix"
                     /note="Vector: Lambda gt11 Sfi-Not; Site_1: EcoRI; Site_2:
                     NotI; Several hundred adult Schistosoma japonicum(Jiangxi,
                     P.R.China, strain),  of mixed sex, were perfused from the
                     mesenteries of experimentally  infected rabbits.
                     Double-strain cDNA synthesized with the mRNA  isolated
                     from adult worm, was inserted into the bacteriophage
                     lambda  gt11 Sfi-Not arms between EcoRI and NotI site of
                     the LacZ gene. The cDNA library was contructed by Chen
                     S.Z. at Nanjing Medical  University, Nanjing, Jiangsu,
                     P.R. China. (see:  Chen Shuzhen, et al. Chinese Journal of
                     Zoonoses 1997,13(6): 23-25)"
BASE COUNT      160 a     67 c    115 g    212 t
ORIGIN
```

```
  Query Match            90.6%;  Score 15.4;  DB 9;  Length 554;
  Best Local Similarity  94.1%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    284 CGGGGTCTTTCCGTCTT 268
```

```
RESULT 39
AW231233/c
LOCUS       AW231233                555 bp    mRNA    linear   EST 10-DEC-1999
DEFINITION  JAYH0020.YL Schistosoma japonicum Lambda gt11 Express library
            Schistosoma japonicum cDNA clone JAYH0020.GY 5', mRNA sequence.
ACCESSION   AW231233
VERSION     AW231233.1  GI:6560529
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 555)
  AUTHORS   Li,F.T., Wu,Z.D. and Yu,X.B.
  TITLE     Expressed sequence tags from adults of Schistosoma japonicum
            (Chinese strain) (Li,F.T.; Wu,Z.D.; Yu,X.B.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Wu ZD
            Department of Parasitology
            Sun-Yat-sen University of Medical Sciences
            BOX 510089, 74# Zhongshen Er Road,Gaungzhou, Guangdong, P.R.China
            Tel: 86-20-87330566
            Fax: 86-20- 87331679
            Email: zdwu62@163.net
            PCR PRimers
            FORWARD: Lambda gt11 Forward Primer
            BACKWARD: Lambda gt11 Reverse Primer
            Seq primer: Lambda gt11 Forward Primer
            High quality sequence stop: 555.
FEATURES             Location/Qualifiers
     source          1. .555
                     /organism="Schistosoma japonicum"
                     /strain="Chinese"
                     /db_xref="taxon:6182"
                     /clone="JAYH0020.GY"
                     /clone_lib="Schistosoma japonicum Lambda gt11 Express
                     library"
                     /sex="Mix"
                     /note="Vector: Lambda gt11 Sfi-Not; Site_1: EcoRI; Site_2:
                     NotI; Several hundred adult Schistosoma japonicum(Jiangxi,
                     P.R.China, strain),  of mixed sex, were perfused from the
                     mesenteries of experimentally  infected rabbits.
                     Double-strain cDNA synthesized with the mRNA  isolated
                     from adult worm, was inserted into the bacteriophage
                     lambda  gt11 Sfi-Not arms between EcoRI and NotI site of
                     the LacZ gene. The cDNA library was contructed by Chen
                     S.Z. at Nanjing Medical  University, Nanjing, Jiangsu,
                     P.R. China. (see:  Chen Shuzhen, et al. Chinese Journal of
                     Zoonoses 1997,13(6): 23-25)"
BASE COUNT      161 a     58 c    107 g    229 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 9;  Length 555;
  Best Local Similarity   94.1%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    368 CGGGGTCTTTCCGTCTT 352


RESULT 40
BE187680/c
LOCUS       BE187680                555 bp    mRNA    linear   EST 22-JUN-2000
DEFINITION  JAYG0068.GYL Schistosoma japonicum Lambda gt11 Express library
            Schistosoma japonicum cDNA clone JAYG0068.GY 5', mRNA sequence.
ACCESSION   BE187680
VERSION     BE187680.1  GI:8666919
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 555)
  AUTHORS   Bian,G., Wu,Z.D. and Yu,X.B.
  TITLE     Expressed sequence tags from adults of Schistosoma japonicum
            (Chinese strain) (Bian,G.; Wu,Z.D.; Yu,X.B.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Wu ZD
            Department of Parasitology
            Sun-Yat-sen University of Medical Sciences
            BOX 510089, 74# Zhongshen Er Road,Gaungzhou, Guangdong, P.R.China
            Tel: 86-20-87330566
            Fax: 86-20- 87331679
            Email: zdwu62@163.net
            PCR PRimers
            FORWARD: Lambda gt11 Forward Primer
            BACKWARD: Lambda gt11 Reverse Primer
            Seq primer: Lambda gt11 Forward Primer
            High quality sequence stop: 555.
FEATURES             Location/Qualifiers
     source          1. .555
                     /organism="Schistosoma japonicum"
                     /strain="Chinese"
                     /db_xref="taxon:6182"
                     /clone="JAYG0068.GY"
                     /clone_lib="Schistosoma japonicum Lambda gt11 Express
                     library"
                     /sex="Mix"
                     /note="Vector: Lambda gt11 Sfi-Not; Site_1: EcoRI; Site_2:
                     NotI; Several hundred adult Schistosoma japonicum(Jiangxi,
                     P.R.China, strain),  of mixed sex, were perfused from the
                     mesenteries of experimentally  infected rabbits.
                     Double-strain cDNA synthesized with the mRNA  isolated
                     from adult worm, was inserted into the bacteriophage
                     lambda  gt11 Sfi-Not arms between EcoRI and NotI site of
                     the LacZ gene. The cDNA library was contructed by Chen
                     S.Z. at Nanjing Medical  University, Nanjing, Jiangsu,
                     P.R. China. (see:  Chen Shuzhen, et al. Chinese Journal of
                     Zoonoses 1997,13(6): 23-25)"
BASE COUNT      160 a     59 c    107 g    229 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 9;  Length 555;
  Best Local Similarity   94.1%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    387 CGGGGTCTTTCCGTCTT 371


RESULT 41
BE819807/c
LOCUS       BE819807                558 bp    mRNA    linear   EST 21-SEP-2000
DEFINITION  JAYB0176.GYL Schistosoma japonicum Lambda gt11 Express library
            Schistosoma japonicum cDNA clone JAYB0176.GY 5', mRNA sequence.
ACCESSION   BE819807
VERSION     BE819807.1  GI:10252041
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 558)
  AUTHORS   Bian,G., Wu,Z.D. and Yu,X.B.
  TITLE     Expressed sequence tags from adults of Schistosoma japonicum
            (Chinese strain) (Bian,G.; Wu,Z.D.; Yu,X.B.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Wu ZD
            Department of Parasitology
            Sun-Yat-sen University of Medical Sciences
            BOX 510089, 74# Zhongshen Er Road,Gaungzhou, Guangdong, P.R.China
            Tel: 86-20-87330566
```

```
            Fax: 86-20- 87331679
            Email: zdwu62@163.net
            PCR PRimers
            FORWARD: Lambda gt11 Forward Primer
            BACKWARD: Lambda gt11 Reverse Primer
            Seq primer: Lambda gt11 Forward Primer
            High quality sequence stop: 558.
FEATURES              Location/Qualifiers
     source           1. .558
                      /organism="Schistosoma japonicum"
                      /strain="Chinese"
                      /db_xref="taxon:6182"
                      /clone="JAYB0176.GY"
                      /clone_lib="Schistosoma japonicum Lambda gt11 Express
                      library"
                      /sex="Mix"
                      /note="Vector: Lambda gt11 Sfi-Not; Site_1: EcoRI; Site_2:
                      NotI; Several hundred adult Schistosoma japonicum(Jiangxi,
                      P.R.China, strain),  of mixed sex, were perfused from the
                      mesenteries of experimentally  infected rabbits.
                      Double-strain cDNA synthesized with the mRNA  isolated
                      from adult worm, was inserted into the bacteriophage
                      lambda  gt11 Sfi-Not arms between EcoRI and NotI site of
                      the LacZ gene. The cDNA library was contructed by Chen
                      S.Z. at Nanjing Medical  University, Nanjing, Jiangsu,
                      P.R. China. (see:  Chen Shuzhen, et al. Chinese Journal of
                      Zoonoses 1997,13(6): 23-25)"
BASE COUNT      162 a     69 c    117 g    210 t
ORIGIN


  Query Match            90.6%;  Score 15.4;  DB 10;  Length 558;
  Best Local Similarity  94.1%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    284 CGGGGTCTTTCCGTCTT 268


RESULT  42
AW191455/c
LOCUS       AW191455                 563 bp    mRNA    linear   EST 20-MAR-2000
DEFINITION  JAA000486.SH3 Adult SjC 7/94 Schistosoma japonicum cDNA 5', mRNA
            sequence.
ACCESSION   AW191455
VERSION     AW191455.1  GI:6467083
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 563)
  AUTHORS   Hu,W., Brindley,P.J. and Feng,Z.
  TITLE     Expressed sequence tags from adults of Schistosoma japonicum (Anhui
            strain) (Hu, Brindley, Feng)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Brindley, P.J.
            Molecular Parasitology Unit
            Queensland Institute of Medical Research
            300 Herston Road, Qeensland 4029, Australia
            Tel: 61 7 3362 0413
            Fax: 61 7 3362 0104
            Email: paulB@qimr.edu.au
            PCR PRimers
            FORWARD: M13 Forward
            BACKWARD: M13 Reverse
            Insert Length: 1   Std Error: 0.00
            Seq primer: T3 Reverse
            High quality sequence start: 124
            High quality sequence stop: 563.
FEATURES              Location/Qualifiers
     source           1. .563
                      /organism="Schistosoma japonicum"
                      /strain="Chinese (Anhui) strain"
                      /db_xref="taxon:6182"
                      /clone_lib="Adult SjC 7/94"
                      /sex="Male and female"
                      /tissue_type="Whole body"
                      /dev_stage="Adult worms"
                      /lab_host="Mouse and rabbit"
                      /note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
                      Xhol I; Several hundred adult Schistosoma japonicum (Anhui
                      , P.R. China, strain), of mixed sex, were perfused from
                      the mesenteries of experimentally infected mice and
                      rabbits at the Queensland Institute of Medical Research,
                      Brisbane, Australia (QIMR), and stored for several months
                      in liquid nitrogen. Subsequently, mRNA was isolated at the
                      QIMR from lysates of these worms by oligo dT
                      chromatography, using a kit from Pharmacia. The mRNA was
                      then shipped to Clontech, Palo Alto, CA, USA, who
                      constructed a cDNA library. First strand synthesis was
                      primed with an oligo-dT-XhoI-primer and synthesized using
                      M-MLV reverse transcriptase. Second strand synthesis was
                      accomplished with RNAse H and T4 DNA polymerase. The
                      double stranded cDNA was ligated to EcoRI linkers,
                      digested with EcoRI and XhoI, and ligated into the
                      phagemid vector lambda ZAP II XR. After construction of
                      this directional library by Clontech, it was returned to
                      the QIMR. During analysis of the library at the QIMR, we
                      have found that a small percentage, 2% to 3%, of the
                      clones contain inserts that appear to be highly homologous
                      to sequences from salmonoid fishes, as determined by
                      homology comparisons using BLAST and by Southern
                      hybridization analysis to genomic DNA from salmon (Sigma
                      Chemical Co., St. Louis, MO) under stringent washing
                      conditions. The remainder of the clones appear to contain
                      S. japonicum sequences."
BASE COUNT      164 a     61 c    107 g    231 t
ORIGIN


  Query Match            90.6%;  Score 15.4;  DB 9;  Length 563;
  Best Local Similarity  94.1%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    390 CGGGGTCTTTCCGTCTT 374


RESULT  43
AW225509/c
LOCUS       AW225509                 585 bp    mRNA    linear   EST 20-MAR-2000
DEFINITION  JAA000526.SH3 Adult SjC 7/94 Schistosoma japonicum cDNA 5', mRNA
            sequence.
ACCESSION   AW225509
VERSION     AW225509.1  GI:6554805
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 585)
  AUTHORS   Hu,W., Brindley,P.J. and Feng,Z.
  TITLE     Expressed sequence tags from adults of Schistosoma japonicum (Anhui
            strain) (Hu, Brindley, Feng)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Brindley, P.J.
            Molecular Parasitology Unit
            Queensland Institute of Medical Research
            300 Herston Road, Qeensland 4029, Australia
            Tel: 61 7 3362 0413
            Fax: 61 7 3362 0104
            Email: paulB@qimr.edu.au
            PCR PRimers
```

```
            FORWARD: M13 Forward
            BACKWARD: M13 Reverse
            Seq primer: T3 Reverse
            High quality sequence stop: 585.
FEATURES              Location/Qualifiers
     source           1. .585
                      /organism="Schistosoma japonicum"
                      /strain="Chinese (Anhui) strain"
                      /db_xref="taxon:6182"
                      /clone_lib="Adult SjC 7/94"
                      /sex="Male and female"
                      /tissue_type="Whole body"
                      /dev_stage="Adult worms"
                      /lab_host="Mouse and rabbit"
                      /note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
                      Xhol I; Several hundred adult Schistosoma japonicum (Anhui
                      , P.R. China, strain), of mixed sex, were perfused from
                      the mesenteries of experimentally infected mice and
                      rabbits at the Queensland Institute of Medical Research,
                      Brisbane, Australia (QIMR), and stored for several months
                      in liquid nitrogen. Subsequently, mRNA was isolated at the
                      QIMR from lysates of these worms by oligo dT
                      chromatography, using a kit from Pharmacia. The mRNA was
                      then shipped to Clontech, Palo Alto, CA, USA, who
                      constructed a cDNA library. First strand synthesis was
                      primed with an oligo-dT-XhoI-primer and synthesized using
                      M-MLV reverse transcriptase. Second strand synthesis was
                      accomplished with RNAse H and T4 DNA polymerase. The
                      double stranded cDNA was ligated to EcoRI linkers,
                      digested with EcoRI and XhoI, and ligated into the
                      phagemid vector lambda ZAP II XR. After construction of
                      this directional library by Clontech, it was returned to
                      the QIMR. During analysis of the library at the QIMR, we
                      have found that a small percentage, 2% to 3%, of the
                      clones contain inserts that appear to be highly homologous
                      to sequences from salmonoid fishes, as determined by
                      homology comparisons using BLAST and by Southern
                      hybridization analysis to genomic DNA from salmon (Sigma
                      Chemical Co., St. Louis, MO) under stringent washing
                      conditions. The remainder of the clones appear to contain
                      S. japonicum sequences."
BASE COUNT      172 a     68 c    119 g    226 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 9;  Length 585;
  Best Local Similarity   94.1%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    305 CGGGGTCTTTCCGTCTT 289


RESULT  44
BF713615/c
LOCUS       BF713615                592 bp    mRNA    linear   EST 02-JAN-2001
DEFINITION  JAYS0031.GYL Schistosoma japonicum Lambda gt11 Express library
            Schistosoma japonicum cDNA clone JAYS0031.GY 5', mRNA sequence.
ACCESSION   BF713615
VERSION     BF713615.1  GI:12013090
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 592)
  AUTHORS   Xiao,S., Wu,Z.D. and Yu,X.B.
  TITLE     Expressed sequence tags from adults of Schistosoma japonicum
            (Chinese strain) (Xiao,S.; Wu,Z.D.; Yu,X.B.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Wu ZD
            Department of Parasitology
            Sun-Yat-sen University of Medical Sciences
            BOX 510089, 74# Zhongshen Er Road,Gaungzhou, Guangdong, P.R.China
            Tel: 86-20-87330566
            Fax: 86-20- 87331679
            Email: zdwu62@163.net
            PCR PRimers
            FORWARD: Lambda gt11 Forward Primer
            BACKWARD: Lambda gt11 Reverse Primer
            Seq primer: Lambda gt11 Forward Primer
            High quality sequence stop: 592.
FEATURES              Location/Qualifiers
     source           1. .592
                      /organism="Schistosoma japonicum"
                      /strain="Chinese"
                      /db_xref="taxon:6182"
                      /clone="JAYS0031.GY"
                      /clone_lib="Schistosoma japonicum Lambda gt11 Express
                      library"
                      /sex="Mix"
                      /note="Vector: Lambda gt11 Sfi-Not; Site_1: EcoRI; Site_2:
                      NotI; Several hundred adult Schistosoma japonicum(Jiangxi,
                      P.R.China, strain),  of mixed sex, were perfused from the
                      mesenteries of experimentally  infected rabbits.
                      Double-strain cDNA synthesized with the mRNA  isolated
                      from adult worm, was inserted into the bacteriophage
                      lambda  gt11 Sfi-Not arms between EcoRI and NotI site of
                      the LacZ gene. The cDNA library was contructed by Chen
                      S.Z. at Nanjing Medical  University, Nanjing, Jiangsu,
                      P.R. China. (see:  Chen Shuzhen, et al. Chinese Journal of
                      Zoonoses 1997,13(6): 23-25)"
BASE COUNT      170 a     65 c    116 g    241 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 10;  Length 592;
  Best Local Similarity   94.1%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    378 CGGGGTCTTTCCGTCTT 362


RESULT  45
AT006807/c
LOCUS       AT006807                606 bp    mRNA    linear   EST 24-JAN-2002
DEFINITION  AT006807 Clonorchis sinensis cDNA Library Clonorchis sinensis cDNA
            clone CS132, mRNA sequence.
ACCESSION   AT006807
VERSION     AT006807.1  GI:18324714
KEYWORDS    EST.
SOURCE      Clonorchis sinensis.
  ORGANISM  Clonorchis sinensis
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Opisthorchiida; Opisthorchiata; Opisthorchioidea; Opisthorchiidae;
            Clonorchis.
REFERENCE   1  (bases 1 to 606)
  AUTHORS   Jisook,L. and Yong,T.
  TITLE     Clonorchis sinensis : ESTs and gene discovery
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Lee Jisook
            Department of Parasitology
            Yonsei University College of Medicine
            134 Sinchon-Dong,Seadaemun-Gu, Seoul 120752, Korea
            Tel: 82-2-361-5299
            Fax: 82-2-363-8676
            Email: prettyoliver@hanmail.net
            Submitted through BRIC(Biological Research Information Center) of
            Korea
            URL: http://bric.postech.ac.kr/.
FEATURES              Location/Qualifiers
     source           1. .606
                      /organism="Clonorchis sinensis"
```

```
                     /db_xref="taxon:79923"
                     /clone="CS132"
                     /clone_lib="Clonorchis sinensis cDNA Library"
                     /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT       145 a      78 c     165 g     218 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 9;  Length 606;
  Best Local Similarity   94.1%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtctt 17
           ||||||||| |||||||
Db     395 CGGGGTCTTTCCGTCTT 379


RESULT  46
AW186560/c
LOCUS       AW186560                 625 bp    mRNA    linear   EST 20-MAR-2000
DEFINITION  JAA000460.SH3 Adult SjC 7/94 Schistosoma japonicum cDNA 5', mRNA
            sequence.
ACCESSION   AW186560
VERSION     AW186560.1  GI:6455877
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 625)
  AUTHORS   Hu,W., Brindley,P.J. and Feng,Z.
  TITLE     Expressed sequence tags from adults of Schistosoma japonicum (Anhui
            strain) (Hu, Brindley, Feng)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Brindley, P.J.
            Molecular Parasitology Unit
            Queensland Institute of Medical Research
            300 Herston Road, Qeensland 4029, Australia
            Tel: 61 7 3362 0413
            Fax: 61 7 3362 0104
            Email: paulB@qimr.edu.au
            PCR PRimers
            FORWARD: M13 Forward
            BACKWARD: M13 Reverse
            Insert Length: 1    Std Error: 0.00
            Seq primer: T3 Reverse
            High quality sequence stop: 625.
FEATURES             Location/Qualifiers
     source          1. .625
                     /organism="Schistosoma japonicum"
                     /strain="Chinese (Anhui) strain"
                     /db_xref="taxon:6182"
                     /clone_lib="Adult SjC 7/94"
                     /sex="Male and female"
                     /tissue_type="Whole body"
                     /dev_stage="Adult worms"
                     /lab_host="Mouse and rabbit"
                     /note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
                     Xhol I; Several hundred adult Schistosoma japonicum (Anhui
                     , P.R. China, strain), of mixed sex, were perfused from
                     the mesenteries of experimentally infected mice and
                     rabbits at the Queensland Institute of Medical Research,
                     Brisbane, Australia (QIMR), and stored for several months
                     in liquid nitrogen. Subsequently, mRNA was isolated at the
                     QIMR from lysates of these worms by oligo dT
                     chromatography, using a kit from Pharmacia. The mRNA was
                     then shipped to Clontech, Palo Alto, CA, USA, who
                     constructed a cDNA library. First strand synthesis was
                     primed with an oligo-dT-XhoI-primer and synthesized using
                     M-MLV reverse transcriptase. Second strand synthesis was
                     accomplished with RNAse H and T4 DNA polymerase. The
                     double stranded cDNA was ligated to EcoRI linkers,
                     digested with EcoRI and XhoI, and ligated into the
                     phagemid vector lambda ZAP II XR. After construction of
                     this directional library by Clontech, it was returned to
                     the QIMR. During analysis of the library at the QIMR, we
                     have found that a small percentage, 2% to 3%, of the
                     clones contain inserts that appear to be highly homologous
                     to sequences from salmonoid fishes, as determined by
                     homology comparisons using BLAST and by Southern
                     hybridization analysis to genomic DNA from salmon (Sigma
                     Chemical Co., St. Louis, MO) under stringent washing
                     conditions. The remainder of the clones appear to contain
                     S. japonicum sequences."
BASE COUNT       187 a      59 c     122 g     257 t
ORIGIN


  Query Match             90.6%;  Score 15.4;  DB 9;  Length 625;
  Best Local Similarity   94.1%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cggggtcttcccgtctt 17
           ||||||||| |||||||
Db     591 CGGGGTCTTTCCGTCTT 575


RESULT  47
BI183250
LOCUS       BI183250                 628 bp    mRNA    linear   EST 10-JUL-2001
DEFINITION  UNL-P-FN-bw-f-08-0-UNL.s1 UNL-P-FN Sus scrofa cDNA clone
            UNL-P-FN-bw-f-08-0-UNL 3', mRNA sequence.
ACCESSION   BI183250
VERSION     BI183250.1  GI:14657659
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 628)
  AUTHORS   Caetano,A.R., Johnson,R.K. and Pomp,D.
  TITLE     Generation and sequence characterization of a normalized cDNA
            library from swine ovarian follicles
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Pomp, D
            Department of Animal Science
            University of Nebraska, Lincoln
            Lincoln, NE 68583-0908, USA
            Tel: 402 472 6416
            Fax: 402 472 6362
            Email: dpomp@unl.edu
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message.
            Seq primer: M13 -29
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .628
                     /organism="Sus scrofa"
                     /strain="University of Nebraska, Lincoln Swine Selection
                     Lines"
                     /db_xref="taxon:9823"
                     /clone="UNL-P-FN-bw-f-08-0-UNL"
                     /clone_lib="UNL-P-FN"
                     /dev_stage="ADULT"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UNL-P-FN
                     library is a normalized library representing porcine
                     ovarian follicles, ranging between 2.0 to 10.0 mm in
                     diameter, collected  during 7 days of the follicular phase
                     of the pig estrous cycle. This  library was derived from
                     the library UNL-P-F2. The tag is a string of  5-6
                     nucleotides present between the Not I site and the
                     oligo-dT track.  The library was constructed as described
                     by Bonaldo, Lennon and Soares,  Genome Research 6: 791-806
                     , 1996.
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TAG_SEQ=None found"
BASE COUNT 99 a 190 c 206 g 127 t 6 others
ORIGIN

Query Match 90.6%; Score 15.4; DB 10; Length 628;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||||| ||||||
Db 265 CGGGGTCTTCTCGTCTT 281

RESULT 48
AQ989715
LOCUS AQ989715 642 bp DNA linear GSS 14-AUG-2000
DEFINITION Rfc00343 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00343, DNA sequence.
ACCESSION AQ989715
VERSION AQ989715.1 GI:9648309
KEYWORDS GSS.
SOURCE Photorhabdus luminescens.
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Photorhabdus.
REFERENCE 1 (bases 1 to 642)
AUTHORS ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE 20378633
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
FEATURES Location/Qualifiers
source 1. .642
/organism="Photorhabdus luminescens"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG00343"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/dev_stage="primary phase variant"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."
BASE COUNT 136 a 183 c 154 g 167 t 2 others
ORIGIN

Query Match 90.6%; Score 15.4; DB 12; Length 642;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17
||||||||| |||||||
Db 138 CGGGGTCTTTCCGTCTT 154

RESULT 49
AW225508/c
LOCUS AW225508 654 bp mRNA linear EST 20-MAR-2000
DEFINITION JAA000525.SH3 Adult SjC 7/94 Schistosoma japonicum cDNA 5', mRNA
sequence.
ACCESSION AW225508
VERSION AW225508.1 GI:6554804
KEYWORDS EST.
SOURCE Schistosoma japonicum.
ORGANISM Schistosoma japonicum
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 654)
AUTHORS Hu,W., Brindley,P.J. and Feng,Z.
TITLE Expressed sequence tags from adults of Schistosoma japonicum (Anhui
strain) (Hu, Brindley, Feng)
JOURNAL Unpublished (1999)
COMMENT Contact: Brindley, P.J.
Molecular Parasitology Unit
Queensland Institute of Medical Research
300 Herston Road, Qeensland 4029, Australia
Tel: 61 7 3362 0413
Fax: 61 7 3362 0104
Email: paulB@qimr.edu.au
PCR PRimers
FORWARD: M13 Forward
BACKWARD: M13 Reverse
Insert Length: 1 Std Error: 0.00
Seq primer: T3 Reverse
High quality sequence stop: 654.
FEATURES Location/Qualifiers
source 1. .654
/organism="Schistosoma japonicum"
/strain="Chinese (Anhui) strain"
/db_xref="taxon:6182"
/clone_lib="Adult SjC 7/94"
/sex="Male and female"
/tissue_type="Whole body"
/dev_stage="Adult worms"
/lab_host="Mouse and rabbit"
/note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
Xhol I; Several hundred adult Schistosoma japonicum (Anhui
, P.R. China, strain), of mixed sex, were perfused from
the mesenteries of experimentally infected mice and
rabbits at the Queensland Institute of Medical Research,
Brisbane, Australia (QIMR), and stored for several months
in liquid nitrogen. Subsequently, mRNA was isolated at the
QIMR from lysates of these worms by oligo dT
chromatography, using a kit from Pharmacia. The mRNA was
then shipped to Clontech, Palo Alto, CA, USA, who
constructed a cDNA library. First strand synthesis was
primed with an oligo-dT-XhoI-primer and synthesized using
M-MLV reverse transcriptase. Second strand synthesis was
accomplished with RNAse H and T4 DNA polymerase. The
double stranded cDNA was ligated to EcoRI linkers,
digested with EcoRI and XhoI, and ligated into the
phagemid vector lambda ZAP II XR. After construction of
this directional library by Clontech, it was returned to
the QIMR. During analysis of the library at the QIMR, we
have found that a small percentage, 2% to 3%, of the
clones contain inserts that appear to be highly homologous
to sequences from salmonoid fishes, as determined by
homology comparisons using BLAST and by Southern
hybridization analysis to genomic DNA from salmon (Sigma
Chemical Co., St. Louis, MO) under stringent washing
conditions. The remainder of the clones appear to contain
S. japonicum sequences."
BASE COUNT 188 a 63 c 124 g 279 t
ORIGIN

Query Match 90.6%; Score 15.4; DB 9; Length 654;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cggggtcttcccgtctt 17

```
          ||||||||| |||||||
Db    624 CGGGGTCTTTCCGTCTT 608


RESULT 50
AI942193/c
LOCUS       AI942193                 658 bp    mRNA    linear   EST 20-MAR-2000
DEFINITION  JAA000355.SH3 Adult SjC 7/94 Schistosoma japonicum cDNA 5', mRNA
            sequence.
ACCESSION   AI942193
VERSION     AI942193.1  GI:5706849
KEYWORDS    EST.
SOURCE      Schistosoma japonicum.
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 658)
  AUTHORS   Hu,W., Brindley,P.J. and Feng,Z.
  TITLE     Expressed sequence tags from adults of Schistosoma japonicum (Anhui
            strain) (Hu, Brindley, Feng)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Brindley, P.J.
            Molecular Parasitology Unit
            Queensland Institute of Medical Research
            300 Herston Road, Qeensland 4029, Australia
            Tel: 61 7 3362 0413
            Fax: 61 7 3362 0104
            Email: paulB@qimr.edu.au
            PCR PRimers
            FORWARD: M13 Forward
            BACKWARD: M13 Reverse
            Insert Length: 1200   Std Error: 0.00
            Seq primer: T3 Reverse
            High quality sequence stop: 658.
FEATURES             Location/Qualifiers
     source          1. .658
                     /organism="Schistosoma japonicum"
                     /strain="Chinese (Anhui) strain"
                     /db_xref="taxon:6182"
                     /clone_lib="Adult SjC 7/94"
                     /sex="Male and female"
                     /tissue_type="Whole body"
                     /dev_stage="Adult worms"
                     /lab_host="Mouse and rabbit"
                     /note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
                     Xhol I; Several hundred adult Schistosoma japonicum (Anhui
                     , P.R. China, strain), of mixed sex, were perfused from
                     the mesenteries of experimentally infected mice and
                     rabbits at the Queensland Institute of Medical Research,
                     Brisbane, Australia (QIMR), and stored for several months
                     in liquid nitrogen. Subsequently, mRNA was isolated at the
                     QIMR from lysates of these worms by oligo dT
                     chromatography, using a kit from Pharmacia. The mRNA was
                     then shipped to Clontech, Palo Alto, CA, USA, who
                     constructed a cDNA library. First strand synthesis was
                     primed with an oligo-dT-XhoI-primer and synthesized using
                     M-MLV reverse transcriptase. Second strand synthesis was
                     accomplished with RNAse H and T4 DNA polymerase. The
                     double stranded cDNA was ligated to EcoRI linkers,
                     digested with EcoRI and XhoI, and ligated into the
                     phagemid vector lambda ZAP II XR. After construction of
                     this directional library by Clontech, it was returned to
                     the QIMR. During analysis of the library at the QIMR, we
                     have found that a small percentage, 2% to 3%, of the
                     clones contain inserts that appear to be highly homologous
                     to sequences from salmonoid fishes, as determined by
                     homology comparisons using BLAST and by Southern
                     hybridization analysis to genomic DNA from salmon (Sigma
                     Chemical Co., St. Louis, MO) under stringent washing
                     conditions. The remainder of the clones appear to contain
                     S. japonicum sequences."
BASE COUNT      190 a     64 c    127 g    277 t
ORIGIN
```

```
  Query Match            90.6%;  Score 15.4;  DB 9;  Length 658;
  Best Local Similarity  94.1%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 cggggtcttcccgtctt 17
          ||||||||| |||||||
Db    620 CGGGGTCTTTCCGTCTT 604


Search completed: September  7, 2002, 19:19:00
Job time: 5885 sec
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